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KINASE CASCADES IN THE REGULATION OF GLUCOSE HOMEOSTASIS

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ABSTRACT

Therapeutic strategies to treat Type 2 Diabetes Mellitus (T2DM) aim at improving muscle insulin sensitivity by either directly modulating, or bypassing defective insulin signaling. Insulin induces metabolic and gene regulatory responses via PI 3-Kinase (PI3K) and Mitogen-Activated Protein Kinase (MAPK) signaling pathways, respectively. MAPK signaling pathways can also be activated by insulin-independent stimuli such as exercise/contraction and stress/hypoxia. AMP-activated Protein Kinase (AMPK) also transduces signals to glucose transport and gene regulatory responses by insulin-independent stimuli. Identifying the molecular mechanisms underlying insulin -dependent and -independent signaling pathways will reveal molecular targets for the pharmacological treatment of insulin resistance.

Glucose induces insulin resistance in skeletal muscle. Glucose sensitive targets in the PI3K signaling pathway were identified in Wistar and Goto-Kakizaki (GK) rats exposed to a 3-hr hyperglycemic infusion. In skeletal muscle, glucose directly activates Phosphoinositide Dependent Kinase 1 (PDK-1) and downstream Protein Kinase C (PKC) isoforms (α/β , δ and ζ) through a mechanism that is independent of changes in PI3K, Protein Kinase B (PKB) and Extracellular signal-Regulated protein Kinase (ERK) phosphorylation. This may account for defects in insulin signaling in non-obese diabetic GK rats, whereby PKC ζ was also activated by hyperglycemia. Thus, hyperglycemia acutely modulates signal transduction and this may account for skeletal muscle insulin resistance at the level of the PI3K pathway.

MAPK activation in skeletal muscle from insulin resistant *ob/ob* mice was measured to determine if insulin-dependent and -independent induction of MAPK signaling is intact in insulin resistant tissue. Insulin action on MAPK was impaired in *ob/ob* mice, whereas contraction-mediated effects were preserved. In addition Phorbol 12-Myristate-13-Acetate (PMA) elicited divergent effects on MAPK signaling in *ob/ob* mice; c-Jun NH2-terminal Kinase (JNK) and ERK phosphorylation were preserved, whereas p38-MAPK phosphorylation was refractory. Thus appropriate MAPK response can be elicited in insulin-resistant skeletal muscle via insulin-independent mechanisms. Exercise and muscle contraction may circumvent aberrant MAPK signaling in insulin-resistant skeletal muscle.

Exercise- and hypoxia-stimulated AMPK activity and glucose transport were measured in skeletal muscle from insulin resistant obese Zucker *fa/fa* rats. An isoform-specific defect in AMPK α 1 activity in response to contraction was observed, which was inconsequential to glucose transport. Thus, AMPK signaling to glucose transport is unaffected by insulin resistance.

Constitutive activation of AMPK can be achieved by AMPK γ 3 missense mutation (R225Q). Transgenic mice overexpressing the R225Q γ 3 mutant form were challenged with a 55% fat diet. Transgenic mice have increased lipid oxidation in the presence of lipid oversupply, which attenuates the expected accumulation of intramuscular triglyceride (TG) content and protects against skeletal muscle insulin resistance. In contrast, ablation of AMPK γ 3 resulted in increased TG content and impaired insulin action. Thus, the muscle specific AMPK γ 3-subunit is a putative target for pharmacological treatment of diet-induced skeletal muscle insulin resistance.

In conclusion insulin signaling defects at the level of PI3K and MAPK pathways appear to contribute to skeletal muscle insulin resistance. Insulin-independent pathways via MAPK and AMPK may prove valuable in the treatment of insulin resistance in T2DM.

Key Words: skeletal muscle, insulin resistance, T2DM, hyperglycemia, high fat diet, glucose transport, PI3K-, MAPK- and AMPK-signaling pathways, AMPK γ 3^{R225Q} mutation.

RESUME

Une des stratégies thérapeutiques de traitement du diabète de type 2 consiste à lutter contre l'insulino-résistance musculaire en ciblant directement des défauts de stimulation du transport du glucose par la voie de signalisation à l'insuline ou par des voies parallèles déclenchées par la contraction musculaire ou le stress. La liaison de l'insuline à son récepteur musculaire allume des cascades de signalisation qui transmettent à la fois des signaux métabolique et mitogénique, grâce aux voies de la PI 3-Kinase et des Mitogen-Activated Protein Kinase (MAPK). Les stimuli non insuliniqes, tels que le stress ou la contraction musculaire, activent les voies des MAPK et de l'AMP-activated Protein Kinase (AMPK) qui stimulent le transport du glucose et/ou des réponses mitogéniques. L'identification et la compréhension des mécanismes moléculaires qui sous-tendent l'activation de ces cascades de signalisation par des stimuli insuliniqes ou non permettront de révéler des cibles thérapeutiques de traitement de l'insulino-résistance musculaire.

L'hyperglycémie est une cause majeure de développement de l'insulino-résistance musculaire. Nous avons identifié des cibles sensibles au glucose en exposant des rats Wistar contrôles et diabétiques Goto-Kakizaki (GK) à une hyperglycémie aiguë. Dans le muscle squelettique, les kinases PDK-1 et PKC α/β , δ et ζ sont activées directement par la glycémie selon un mécanisme indépendant de l'activation des kinases PI3K, PKB et ERK. Chez les rats GK, la PKC ζ est aussi activée par une hyperglycémie aiguë. Dans le muscle, le niveau de la glycémie module donc l'activité de protéines de signalisation et cela pourrait expliquer les défauts dans la voie de signalisation de la PI3K.

Pour déterminer si la voie des MAPK est intacte dans un modèle d'insulino-résistance musculaire, nous avons mesuré l'état d'activation de kinases comme JNK, p38-MAPK et ERK dans le muscle squelettique des souris obèses *ob/ob* en réponse à des stimuli insulino-sensibles ou non. Chez ces souris, la réponse insuliniqes des MAPK est défectueuse alors qu'elles sont normalement activées par la contraction musculaire. De même l'activation par le Phorbol 12-myristate-13-acetate (PMA) de la p38-MAPK est inexistante alors que celle de JNK et ERK est intacte. Ces défauts dans la cascade de signalisation des MAPK pourraient participer à l'insulino-résistance musculaire des souris *ob/ob*. Cependant des stimuli tels que le PMA et la contraction musculaire seraient susceptibles de combattre ces défauts.

Nous avons également étudié le rôle potentiel de sous unités de l'AMPK dans deux modèles de résistance à l'insuline. L'effet de l'hypoxie et de la contraction musculaire sur le transport du glucose a été mesuré dans un modèle de rats Zucker *fa/fa*. Nous avons identifié un défaut d'activation de l'isoforme $\alpha 1$ de l'AMPK en réponse à la contraction musculaire dans le muscle squelettique de ces rats, sans altération du transport du glucose. Ainsi l'activation du transport du glucose par l'AMPK est intacte dans le muscle squelettique de ce modèle animal. Par ailleurs, le rôle de la sous unité $\gamma 3$ de l'AMPK a été évalué chez des souris nourries avec un régime hyperlipidique et qui surexpriment dans le muscle squelettique, une forme constitutivement active de cette sous unité $\gamma 3$. Ces souris montrent une capacité accrue d'oxydation des lipides, réduisant l'accumulation de triglycérides intramusculaires et prévenant le développement de l'insulino-résistance. Par contre, les souris dont le gène $\gamma 3$ a été invalidé sont résistantes à l'insuline, et stockent autant de triglycérides que les souris témoins au même régime hyperlipidique. Ainsi la sous-unité $\gamma 3$ de l'AMPK est une cible potentielle pour lutter contre l'insulino-résistance musculaire induite par un régime hyperlipidique.

En conclusion, l'insulino-résistance musculaire peut s'expliquer par des défauts de signalisation dans les voies de la PI3K et des MAPK. L'activation des cascades de signalisation de l'AMPK et des MAPK en réponse à des stimuli, tels que la contraction musculaire ou le PMA, offrent des possibilités de combattre cette résistance à l'insuline.

Mots-clés : muscle squelettique, insulino-résistance, diabète de type 2, hyperglycémie, régime hyperlipidique, transport du glucose, voie de signalisation des PI3K, MAPK et de l'AMPK, mutation AMPK $\gamma 3^{R225}$.

LIST OF PUBLICATIONS

This thesis is based on the following papers, which are referred to in the text by their respective Roman numerals, and additional unpublished work.

- I. Steiler T.L., Galuska D., Leng Y., Chibalin A.V., Gilbert M. and Zierath J.R. Effect of hyperglycemia on signal transduction in skeletal muscle from diabetic Goto-Kakizaki rats. *Endocrinology* 144: 5259-5267, 2003.
- II. Leng Y., Steiler T.L. and Zierath J.R. Effects of insulin, contraction and phorbol esters on mitogen-activated protein kinase signaling in skeletal muscle from lean and *ob/ob* mice. *Diabetes* 53: 1436-1444, 2004.
- III. Barnes B.R.*, Ryder J.W.*, Steiler T.L., Fryer L.G.D., Carling D. and Zierath J.R. Isoform-specific regulation of 5' AMP-activated protein kinase in skeletal muscle from obese Zucker (*fa/fa*) rats in response to contraction. *Diabetes* 51: 2703-2708, 2002.
- IV. Barnes B.R.*, Marklund S.*, Steiler T.L.*, Walter M., Hjälm G., Amarger V., Mahlapuu M., Leng Y., Johansson C., Galuska D., Lindgren K., Åbrink M., Stapleton D., Zierath J.R. and Andersson L. The 5'-AMP-activated protein kinase γ 3 isoform has a key role in carbohydrate and lipid metabolism in glycolytic skeletal muscle. *J. Biol. Chem.* 279: 38441-38447, 2004.

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ABBREVIATIONS

ACC	Acetyl CoA carbonylase
AICAR	5-aminoimidazole-4-carboxamide riboside
AMPK	AMP-activated protein kinase
AMPKK	AMP-activated protein kinase kinase
AMP/ATP	Adenosine-mono-/tri-phosphate
AS160	<i>Akt</i> substrate of 160 kDa
BSA	Bovine serum albumine
bw	body weight
DAG	Diacylglycerol
EDL	Extensor digitorum longus
ERK	Extracellular signal-regulated protein kinase
FFA	Free fatty acid
GK Rat	Goto-Kakizaki rat
GLUT4	Glucose transporter 4
GS	Glycogen synthase
IR	Insulin receptor
IRS	Insulin receptor substrate
JNK	c-jun NH2-terminal kinase
KHB	Krebs henseleit buffer
MAPK	Mitogen-activated protein kinase
MCD	Malonyl CoA decarboxylase
MEK	MAPK kinase
MEKK	MAPK kinase kinase
PDK-1	Phosphoinositide dependent kinase-1
PH	Pleckstrin homology
PI	Phosphatidylinositol
PI 3-Kinase	Phosphatidylinositol 3-kinase
PKB	Protein kinase B
c, n, aPKC	conventionnal, novel, atypical protein kinase C
PMA	Phorbol 12-myristate-13-acetate
Prkag3 ^{-/-}	AMPK γ 3 knock out mouse model
PS	Phosphatidylserine
RIA	Radioimmunoassay
SH2	Src homology domain 2
TBST	Tris buffer saline tween
TG	Triglyceride
Tg-Prkag3 ^{wt}	Transgenic mouse overexpressing wild type AMPK γ 3
Tg-Prkag3 ^{225Q}	Transgenic mouse overexpressing mutant (R225Q) AMPK γ 3
T2DM	Type 2 diabetes mellitus

INTRODUCTION

The number of patients diagnosed with Type 2 Diabetes Mellitus (T2DM) is growing at an astronomical rate. Insulin resistance is a characteristic feature of the disease, and leads to altered whole body glucose homeostasis (DeFronzo et al. 1992) and impaired skeletal muscle glucose transport (Zierath et al. 1994; Rothman et al. 1995). Insulin-induced glucose transport in skeletal muscle is mediated by transmembrane glucose transport that occurs in response to Glucose Transporter 4 (GLUT4) translocation from an intracellular pool to the plasma membrane. While GLUT4 expression in T2DM patients is unchanged compared to controls (Garvey et al. 1992; Andersen et al. 1993), insulin-stimulated GLUT4 content in plasma membrane and GLUT4 translocation in skeletal muscle from insulin resistant diabetic patients are reduced (Zierath et al. 1996; Garvey et al. 1998). Therefore the defects along the glucose transport process might lie in the insulin signaling pathway (Vogt et al. 1992; Garvey et al. 1998).

Insulin Signaling Pathways

Glucose transport, activation of glycogen or protein synthesis and initiation of specific gene transcription are regulated via intracellular signaling pathways that are activated when insulin binds to its receptor. Phosphatidylinositol 3-Kinase (PI3K) and Mitogen Activated Protein Kinase (MAPK) pathways are the two major pathways activated in response to insulin receptor phosphorylation.

The insulin receptor (IR) belongs to a large family of growth factor receptors with intrinsic tyrosine kinase activity and it is composed of two α and two β subunits. Insulin binds to the extracellular α -subunits, whereas transmembrane β -subunits contain the tyrosine kinase activity. Following insulin stimulation, IR undergoes autophosphorylation on multiple tyrosine residues (Kasuga et al. 1983), leading to receptor kinase activation and subsequent tyrosine phosphorylation of a family of IR substrate (IRS) proteins.

IRS are commonly referred to as docking proteins, since several other proteins bind to phosphorylated IRS (White 1997). To date, four different IRS molecules have been cloned and the predominant isoforms expressed in skeletal muscle are IRS-1 and IRS-2 (White 1997). IRS are involved in transducing metabolic and mitogenic effects of insulin (Araki et al. 1994, Withers et al. 1998). IRS are phosphorylated on multiple tyrosine residues by IR tyrosine kinase at YXXM and YMXM motifs. Once phosphorylated, IRS serve as docking sites for molecules containing Src homology 2 domains (SH2), namely PI3K and the MAPK activator, Grb2.

The PI3K Signaling Cascade

PI3K is a lipid kinase that associates with IRS-1 and signals to glucose transport following insulin stimulation (Cheatham et al. 1994). PI3K consists of a 110-kDa catalytic subunit and an 85-kDa regulatory subunit with two SH2 domains. Binding of the SH2 domains with the two YMXM motifs present in IRS-1, markedly stimulates PI3K activity, as measured in anti-IRS-1 or anti-phosphotyrosine immunoprecipitates (Herbst et al. 1995). PI3K phosphorylates phosphatidylinositol (PI), PI 4-phosphate and PI 4,5-bisphosphate at position D-3 of the inositol ring

generating respectively PI 3-phosphate, PI 3,4-bisphosphate (PIP₂) and PI 3,4,5-triphosphate (PIP₃).

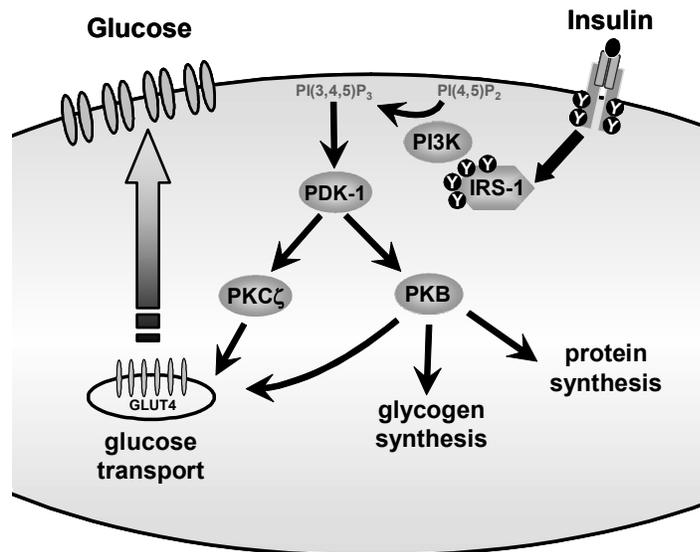


Figure 1. IRS-1 signaling cascade to glucose transport

PIP₃ is an allosteric activator of Phosphoinositide-Dependent Kinase 1 (PDK-1). PDK-1 is a serine/threonine kinase that activates Protein Kinase B (PKB) and Protein Kinase C (PKC) via direct phosphorylation of key sites in their activation loop (Mora et al. 2004). PDK-1 is rate-limiting for insulin-stimulated glucose transport and subsequent GLUT4 translocation (Bandyopadhyay et al. 1999; Grillo et al. 1999). Activation of PDK-1 remains controversial, mainly because conclusions have been drawn from cell culture models and *in vivo* data is lacking. In resting cells, PDK-1 appears to be constitutively active (Mora et al. 2004). However additional insulin-stimulated serine (Casamayor et al. 1999) and tyrosine (Park et al. 2001) phosphorylation events may occur that seem to be associated with substantial increases in PDK-1 activity (Chen et al. 2001). Recruitment of PDK-1 to the plasma membrane also seems to be necessary for full activation of the enzyme, a finding consistent with insulin-stimulated plasma membrane translocation of downstream PDK-1 substrates (Egawa et al. 2002).

The downstream pathways by which insulin-stimulated PI3K activity leads to GLUT4 translocation involve activation of the serine/threonine kinases PKB and PKC. Several lines of evidence indicate that PKB functions downstream of PI3K (Burgering et al. 1995; Kohn et al. 1996; Franke et al. 1997) and mediates insulin signaling to glucose transport (Cho et al. 2001; Jiang et al. 2003, Katome et al. 2003). PKB is encoded by *Akt* proto-oncogene and is defined by an NH₂-terminal regulatory domain and a pleckstrin homology (PH) domain required for protein-protein interaction (Downward 1995). To date, three PKB isoforms have been cloned. PKBα encoded by *Akt1*, and PKBβ encoded by *Akt2*, are the predominant isoforms expressed in skeletal muscle (Hanada et al. 2004). Binding of PI3K products to the PH domain results in translocation of PKB to the plasma membrane, where it is activated through phosphorylation by upstream kinases including PDK-1. Full activation of PKB requires phosphorylation of threonine 308 and serine 473 by PDK-1 (Alessi et al. 1996) and leads to its homodimerisation (Hanada et al. 2004).

PKB β plays a major role in regulating glucose homeostasis and insulin-stimulated glucose transport in EDL (Cho et al. 2001). Once activated, PKB phosphorylates downstream substrates, such as the newly identified Akt Substrate of 160 kDa (AS160). AS160 is a 160 kDa protein that is activated and redistributed to the plasma membrane following phosphorylation by PKB (Kane et al. 2002). In adipocytes, AS160 mediates insulin-stimulated PKB signaling to glucose transport possibly via regulation of GLUT4 endocytosis (Sano et al. 2003; Zeigerer et al. 2004). AS160 is also expressed in rat skeletal muscle and phosphorylated in response to insulin and contraction (Bruss et al. 2005), suggesting a potentially similar role in this tissue. In addition to glucose transport, PKB mediates the effect of insulin on glycogen synthesis via glycogen synthase kinase 3 phosphorylation (Markuns et al. 1999), and lipid metabolism via phosphodiesterase 3B phosphorylation (Wijkander et al. 1998).

Other downstream candidates in the insulin signaling pathway to glucose transport include members of the PKC family. PKC are important regulators of cell growth, differentiation and metabolism (Hug et al. 1993; Dekker et al. 1994; Bandyopadhyay et al. 1997). The PKC family consists of at least 12 highly conserved and ubiquitously expressed serine/threonine kinase isotypes that are classified into three subfamilies on the basis of their enzymatic properties, including conventional cPKC (α , β and γ), novel nPKC (δ , ϵ , η and θ) and atypical aPKC (λ and ζ) isoforms (Newton 1995). All PKC isoforms are expressed in skeletal muscle (Puceat et al. 1996). PKC are characterized by their dependence upon lipids for activity. Specifically, the conventional and novel isotypes display a physiological role for diacylglyceride (DAG), which is necessary for translocation of PKC to cellular membranes (Newton 1995). Phorbol ester can substitute for DAG in stimulating and prolonging PKC activity (Nishizuka 1995). In addition to DAG regulation, all PKC isozymes require phosphatidyl serine (PS), an acidic lipid located exclusively on the cytoplasmic face of membranes, whereas nPKC require Ca^{2+} for optimal activity (Newton 1995). All PKC isoforms can be activated by PDK-1 via phosphorylation on specific serine/threonine residues in the activation loop (Mora et al. 2004). To date, the isoform specific function of PKC isoforms and the potential role of these kinases in T2DM pathogenesis remain largely undefined.

PKC positively and negatively mediate insulin action via isoform specific activation. Indeed PKC- δ and - ζ are implicated in acute insulin-stimulated glucose transport (Bandyopadhyay et al. 1997; Kotani et al. 1998, Braiman et al., 1999), whereas PKC- α and - β act as negative feedback regulators of insulin signaling (Standaert et al. 1999; Letiges et al. 2002). Recent evidence suggests there is an isoform specific role of PKC isoforms in the regulation of insulin action. The PKC δ -isoform is involved in skeletal muscle insulin-stimulated glucose transport via direct interaction with the IR (Braiman et al. 2001), independently from PI3K, while the PKC ζ -isoform mediates insulin-stimulated glucose transport through a PI3K-dependent mechanism (Standaert et al. 1996, Ishizuka et al., 2001). PKC ζ has also been hypothesized to stimulate glucose transport by an insulin-independent pathway (Hansen et al. 1997). Indeed physiological exercise (Perrini et al. 2004), the adenosine analogue 5-aminoimidazole-4-carboxamide riboside (AICAR) and phorbol ester activate PKC ζ , possibly via MAPK-(Chen et al. 2002) and/or AMP-activated protein Kinase (AMPK)-mediated mechanisms (Chen et al. 2002).

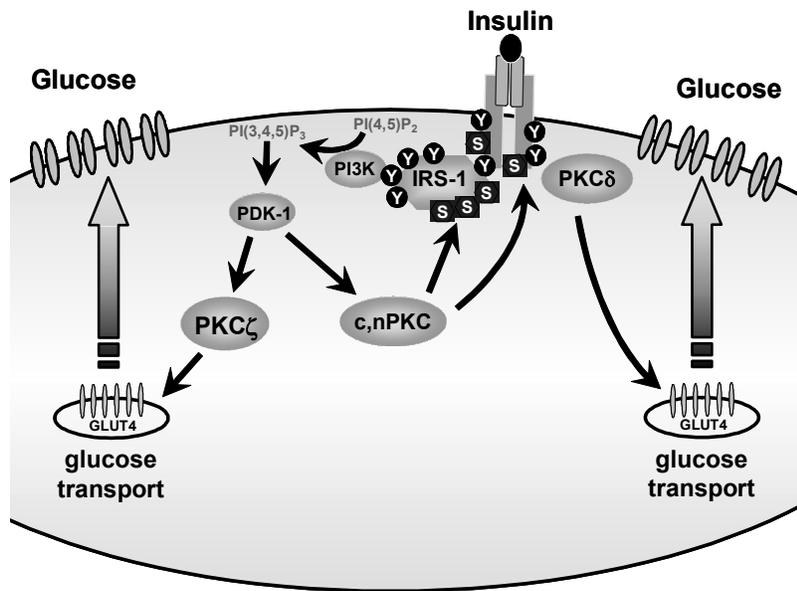


Figure 2. PKC isoform-specific regulation of insulin signaling

Insulin regulation of glucose transport is mediated by PKC, which elicit isoform-specific opposing effects on glucose transport. Insulin activation of PKC- δ and - ζ upregulates GLUT4 translocation to the plasma membrane and subsequent glucose transport activity whereas insulin activation of c,nPKC downregulates the process.

PKC attenuation of insulin signaling involves PKC-induced serine phosphorylation of IR and IRS-1 (Bollag et al. 1986; Chin et al. 1993). Increased IR and IRS-1 serine phosphorylation results in reduced IRS-1 tyrosine phosphorylation and PI3K activity following insulin stimulation (Newton 1995, Li et al., 2004). Increased IR and IRS-1 serine phosphorylation rapidly suppresses insulin-stimulated glucose transport (Tanti et al. 1994). Thus PKC appear to attenuate insulin action via IR desensitization under normal physiological conditions. This may be of particular importance in the case of T2DM and obesity where insulin resistance has been associated with aberrant PKC activation.

The PI3K signaling pathway plays a key role in transmitting insulin signaling to glucose transport in skeletal muscle. In humans and rodents, insulin-stimulated glucose uptake occurs in response to GLUT4 translocation from an intracellular pool to the plasma membrane (Guma et al. 1995). GLUT4 is the major glucose transporter isoform expressed in skeletal muscle (Charron et al. 1989) and it catalyzes a rate limiting step for glucose uptake and metabolism (Marshall et al. 1994). In light of these results, functional defects in any of the IRS-1/PI3K signal transducers may account for impairments in glucose uptake and metabolism in diabetic skeletal muscle.

The MAPK Signaling Cascade

MAPK are conserved and ubiquitously expressed serine/threonine kinases involved in the transduction of externally derived signals regulating cell growth, division, differentiation, adaptation and apoptosis. Mammalian cells contain at least three major classes of MAPK: the Extracellular signal Regulated Kinases 1 and 2 (ERK1/2), c-jun N-terminal Kinase (JNK) and p38-MAPK. MAPK activation is regulated via a series of parallel kinase cascades organized into multiproteic

complexes, with each pathway comprising three kinases that successively phosphorylate and activate the downstream component. In the ERK1/2 kinase pathway, the proximal Raf-1 (a MAPK Kinase Kinase or MEKK) phosphorylates and activates MAPK Kinase 1 and 2 (MEK 1 and 2). MEK1 and 2 are dual threonine/tyrosine kinases that in turn phosphorylate and activate ERK1/2. Regulation of the JNK and p38 MAPK modules also occurs via a MEK and MEKK phosphorylation cascade, mimicking that of the ERK1/2 cascade (Pearson et al. 2001).

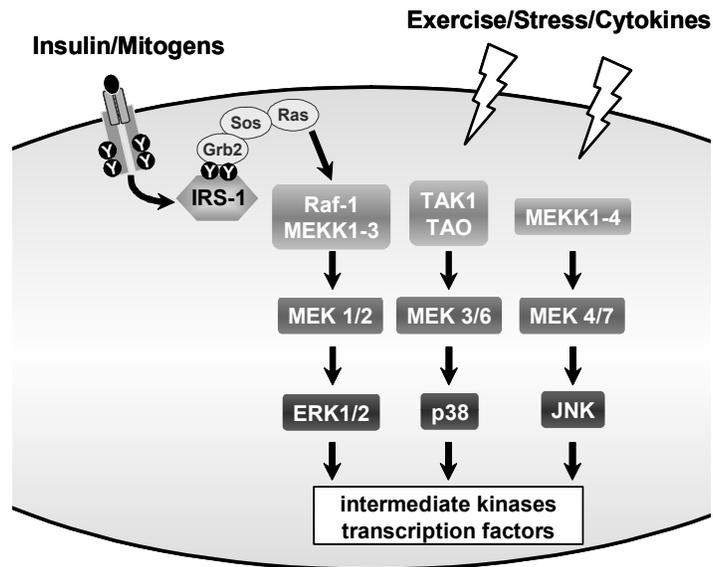


Figure 3. MAPK signaling cascade

MAPK signaling enhances gene expression via phosphorylation of a wide variety of transcription factors and intermediary kinases. Transcription factors can be regulated by all three MAPK or by one in particular. For instance, ERK1/2 and p38-MAPK phosphorylate serum response factor accessory protein-1 (Janknecht et al. 1995, Whitmarsh et al., 1997), whereas all three MAPK phosphorylate Elk-1 (Cavigelli et al. 1995, Kim et al., 1997, Whitmarsh et al., 1997). p38-MAPK phosphorylates Myosin Enhancing Factor 2 (MEF2) (Zhao et al. 1999), while JNK modulates c-jun (Janknecht et al. 1995), Signal Transducer and Activator of Transcription 3 (STAT3) (Lim et al. 1999) and Nuclear Factor Activated T-cell (NFAT) (Chow et al. 2000). STAT3 has recently been implicated in the regulation of hepatic gluconeogenesis (Inoue et al. 2004), whereas MEF2 and NFAT mediate skeletal muscle fiber type (Chin et al. 1998).

Intermediary kinases can also be phosphorylated by one or several MAPK. ERK1/2 and p38-MAPK phosphorylate mitogen- and stress-activated protein kinase-1 and -2 (Deak et al. 1998) and MAPK activated protein kinase-2 and -3 (Cuenda et al. 1995). ERK1/2 specifically modulates p90 ribosomal S6 kinase (Xing et al. 1996), whereas JNK specifically phosphorylates IRS-1 (Lee et al. 2003). Activation of the JNK pathway interferes with insulin action via serine phosphorylation of IRS-1 (Aguirre et al. 2000) and subsequent downregulation of tyrosine induced-insulin intracellular signaling (Lee et al. 2003). Thus, disruption of the JNK-mediated IRS-1 serine phosphorylation may be a potential treatment strategy for insulin resistance.

The MAPK signaling cascade allows for transduction and/or amplification of highly specialized signals. MAPK pathways transduce insulin-dependent and -independent signaling to gene regulatory responses. ERK1/2 is traditionally a mitogenic signal transducer, whereas p38-MAPK and JNK also sense stress-related signals. Indeed the ERK1/2 module is mainly activated by hormones including insulin, growth factors, serum; G-protein coupled receptor ligands, and transforming agents, whereas p38-MAPK and JNK modules are also recruited by cytokines, cellular stress such as osmotic shock, heat shock and DNA interfering agents and protein synthesis (Pearson et al. 2001).

Insulin-dependent MAPK signaling

Insulin induces mitogenic responses via activation of all three MAPK modules (Moxham et al. 1996; Somwar et al. 2000). Grb2-mediated ERK1/2 activation is a well- characterized pathway in this regard. Grb2 is a SH2 domain-containing protein that associates with IRS-1 (Skolnik et al. 1993). Following insulin stimulation, Grb2 interacts with Son of sevenless (Sos) via its SH3 domains (Leevers et al. 1994). Recruitment of Sos to the plasma membrane results in Ras GDP↔GTP exchange and subsequent activation (Downward 1996). Once activated, Ras interacts with Raf-1 and turns on MAPK signaling to ERK1/2 (Marais et al. 1995). Insulin activation of MAPK might also occur via a Ras-independent, PKC-dependent mechanism (Formisano et al. 2000; Letiges et al. 2002). In skeletal muscle the upstream MEKK activating mechanism of MAPK remains undefined.

Insulin-independent MAPK signaling

Exercise training has beneficial effects on whole body insulin sensitivity (Houmard et al. 1993; Hughes et al. 1993). In response to regular contractile activity or physical exercise, skeletal muscle undergoes profound adaptive changes in regard to metabolic and structural properties (Eriksson et al. 1973). These changes might be mediated by increased protein expression of GLUT4 and key insulin signaling enzymes (Ren et al. 1995; Chibalin et al. 2000). However the mechanism involved in exercise-induced skeletal muscle adaptation is unclear. MAPK might be intracellular messengers linking skeletal muscle activity to adaptation. Indeed, exercise activates MAPK in human (Aronson et al., 1997b) and rat (Goodyear et al., 1996; Aronson et al., 1997a) skeletal muscle and in cultured cells, MAPK activation results in cell growth and differentiation (Chen et al. 2001).

MAPK signaling and muscle fiber type

Insulin-stimulated glucose transport is positively correlated with slow- vs. fast-twitch skeletal muscle fibers (Hickey et al. 1995). Insulin action in skeletal muscle occurs through fiber-type specific activation of components of the insulin signaling cascade (Song et al. 1999). Skeletal muscle fiber-type transformation is associated with improved insulin sensitivity (Ryder et al. 2003). Moreover MAPK signaling pathways are differentially activated and expressed in slow- and fast-twitch muscle fibers (Wojtaszewski et al. 1999; Wretman et al. 2000). Thus MAPK fiber-type-specific signaling may be of importance in the search for means to improve insulin sensitivity in insulin resistant states. However little to no data is available on muscle fiber type specific mitogenic effects of insulin-dependent and -independent stimuli on MAPK in normal and insulin resistant animal models.

The AMPK Signaling Cascade

Exercise/contraction and stress/hypoxia are insulin-independent stimuli that also signal to glucose transport. Understanding the molecular mechanisms underlying insulin-independent activation of muscle glucose transport might reveal potential therapeutic targets for the treatment of insulin resistance. AMPK was recently identified as a key mediator of exercise-stimulated glucose transport (Hayashi et al. 1998; Musi et al. 2001). In skeletal muscle, AMPK monitors the energy status of the cell by sensing changes in AMP:ATP and Creatine:Cr-P ratios. Thus energy depleting stimuli, such as exercise and contraction or pathophysiological hypoxia, activate AMPK. The resulting effect is energy repletion via stimulation of glucose transport and fuel utilization through increased fatty acid oxidation and inhibition of fat storage (Winder 2001).

AMPK is a heterotrimeric complex comprising a catalytic α -subunit and two regulatory β - and γ -subunits. Two isoforms encode the α - and β -subunits, and three isoforms encode the γ -subunit. Although $\alpha 1$, $\beta 1$ and $\gamma 1$ are the predominant isoforms in most cells; skeletal muscle also expresses $\alpha 2$, $\beta 2$, $\gamma 2$ and $\gamma 3$ (Kemp et al. 2003). Specific expression of $\gamma 3$ in glycolytic skeletal muscle fibers (Mahlpuu et al. 2004) provides evidence that the combination of different isoforms may have specific functions in skeletal muscle. Indeed identification of mutated forms of all three γ -subunits shows similarities and differences in the metabolic phenotype (Milan et al. 2000).

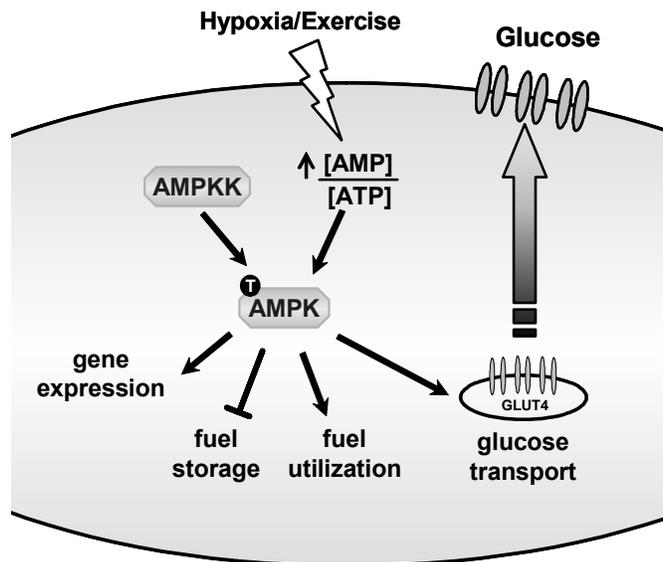


Figure 4. AMPK signaling cascade

Activation of AMPK occurs via both allosteric activation by AMP and phosphorylation of threonine 172 in the activation loop of the catalytic α -subunit by upstream AMPK Kinase (AMPKK). The tumor suppressor LKB1 was recently identified as the major AMPKK (Woods et al. 2003) but dominant-negative expression of LKB1 does not lead to complete loss of basal AMPK activity suggesting that other AMPKK still remain to be identified.

Pharmacological activation of AMPK can be achieved in response to AICAR. AICAR is an adenosine analog that is taken up into cells and converted by adenosine kinase to the monophosphorylated nucleotide 5-aminoimidazole-4-carboxamide-1-D-

ribofuranosyl-5'-monophosphate (ZMP). ZMP mimics all of the activating effects of AMP on the AMPK system, although it is less potent than AMP itself. AICAR stimulates AMPK and increases glucose uptake by promoting GLUT4 translocation to the cell surface in rodent (Musi et al. 2003) and human skeletal muscle (Koistinen et al. 2003). Thus, activation of AMPK may be one strategy to bypass defective insulin signaling to glucose transport.

Numerous downstream targets of AMPK have been identified. These proteins are important for glucose and lipid metabolism and include 6-phosphofructo-2-kinase 2, glycogen synthase (GS), IRS-1, 3-hydroxy-3-methylglutaryl-coenzyme A reductase, hormone sensitive lipase, acetyl-coenzyme A carboxylase (ACC), glycerol phosphate acyl transferase and malonyl CoA decarboxylase (MCD) (Hardie 2003). AMPK regulation of gene involved in fuel metabolism might account for exercise-induced improvements in skeletal muscle insulin sensitivity (Musi et al. 2003).

Targeting AMPK for the treatment of T2DM

AMPK activation causes many metabolic changes that should be beneficial for subjects with T2DM. This is supported by evidence that chronic activation of AMPK via AICAR treatment improves glucose and lipid homeostasis, and insulin resistance in animal models of diabetes and obesity (Iglesias et al. 2002; Olsen et al. 2002). Leptin activates AMPK in skeletal muscle, thereby increasing fatty acid oxidation (Steinberg et al. 2003), whereas adiponectin activates AMPK in liver and muscle to stimulate glucose and fatty acid usage, and to inhibit hepatic glucose production (Tomas et al. 2002; Yamauchi et al. 2002). Furthermore AMPK mediates the action of the antidiabetic drugs metformin (Musi et al. 2002) and rosiglitazone (Fryer et al. 2002), indicating that AMPK activators may play a role as antidiabetic agents. The underlying mechanisms for these effects remain largely undefined. Some evidence suggests that there is cross-talk between AMPK and insulin signaling pathways. Indeed AMPK activation has been observed simultaneously with activation of PKC ζ and ERK1/2 under insulin-independent activation of glucose transport (Chen et al. 2002). AMPK also phosphorylate IRS-1 on serine 789 in C2C12 myotubes, which correlates with an increase in IRS-1 associated PI3K activity (Jakobsen et al. 2001).

Type 2 Diabetes Mellitus and Skeletal Muscle Insulin Resistance

Recent studies in animal models (Folli et al. 1993; Saad et al. 1993) and isolated tissues from T2DM patients (Björnholm et al., 1997; Krook et al., 2000) provide evidence that genetic and environmental factors regulate insulin signaling by changing the function, or covalent modifications of proteins involved in the intracellular network of insulin action.

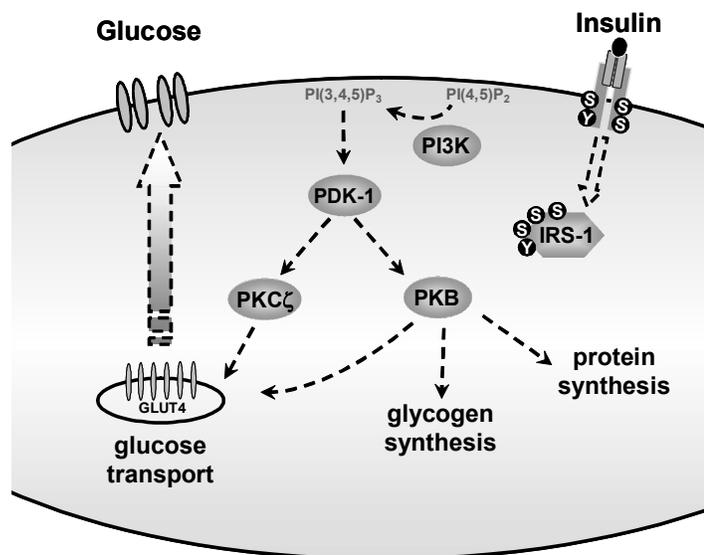


Figure 5. Defects in PI3K signaling

Defects in the early steps of insulin signaling pathways

Several studies report that a decrease in IR and IRS-1 protein phosphorylation is associated with reduced PI3K activity in skeletal muscle from T2DM patients (Björnholm et al., 1997) and obese insulin resistant subjects (Goodyear et al. 1995). However reduced phosphorylation of both IR and IRS-1 was unrelated to changes in protein expression (Björnholm et al., 1997; Zierath et al., 1998). In contrast reduced number and activity of IR has been observed in skeletal muscle and liver from *ob/ob* mice (Kahn et al. 1973; Soll et al. 1975). Genetic analysis also confirms these findings: IRS-1 exhibits multiple natural polymorphisms that are more common in T2DM patients than in control subjects. The G972R for instance, is associated with decreased insulin sensitivity during the oral glucose tolerance test and homozygotes for the codon exhibits diabetes (Almind et al. 1993; Laakso et al. 1994). Further studies revealed a specific defect in binding of the p85 regulatory subunit of PI3K to IRS-1 resulting in reduced IRS-1 associated PI3K activity (Almind et al. 1996). Interestingly subsequent PDK-1 activation is unaltered in T2DM patients (Kim et al. 2003).

Recent evidence suggests that reduced tyrosine phosphorylation of IR and IRS-1 is linked to increased serine phosphorylation of these targets (Tanti et al. 1994; Kanety et al. 1995), thereby providing a mechanism for impaired insulin-stimulated glucose transport (Le Marchand-Brustel et al., 2003). Indeed aberrant serine phosphorylation of IRS-1 has been noted in insulin resistant T2DM patients (Bouzakri et al. 2003) and obese (Eckel et al. 1985) or high fat-fed animal models (Schmitz-Peiffer et al., 1997; Schmitz-Peiffer 2000). Aberrant IRS-1 tyrosine and serine phosphorylation may directly interfere with insulin activation of downstream PI3K and MAPK signaling cascades.

Defects in PI3K signaling

PKB is a downstream target of PI3K (Franke et al. 1995) through PIP₃ and PDK-1 (Alessi et al. 1997). PKB is stimulated in human skeletal muscle in response

to either *in vitro* (Krook et al. 1998) or *in vivo* (Kim et al. 1999) insulin exposure and the activation is sustained throughout the insulin stimulation. Insulin-induced PKB phosphorylation (up to 60 nM) is reduced in skeletal muscle from T2DM patients compared to control subjects (Krook et al. 1998). At lower, more physiological insulin concentrations, PKB phosphorylation and activation is however comparable between T2DM patients and lean controls (Kim et al. 1999), despite severely impaired PI3K and GS activity (Vaag et al. 1992). Aberrant PKB activation is also controversial in insulin resistant animal models (Krook et al. 1997; Kim et al. 2000; Kanoh et al. 2001; Standaert et al. 2004). Thus, the role of PKB in the development of insulin resistance in skeletal muscle remains unclear.

PKC are downstream targets of PI3K and can be activated following insulin stimulation. Insulin activation of PKC isoforms leads to positive and negative modulation of its signal. Aberrant isoform specific PKC translocation, activation and protein expression have been reported in skeletal muscle from insulin resistant animal models. For example, the positive insulin signal transducers, PKC- δ and - ζ , are down-regulated in insulin resistant animal models (Avignon et al. 1996; Schmitz-Peiffer et al. 1997), indicating that these isoforms are candidates leading to impaired glucose uptake and metabolism in diabetes. Similarly in human, insulin-stimulated PKC ζ is impaired in skeletal muscle from glucose intolerant, diabetic (Beeson et al. 2003) and insulin resistant obese (Kim et al. 2003) subjects.

A number of studies have linked increased c,nPKC activation in skeletal muscle to diminished insulin sensitivity in humans (Itani et al. 2000) and animals models of T2DM (Schmitz-Peiffer 2000). Isoform specific defects in skeletal muscle have been revealed through the use of PKC isoform-specific antibodies. PKC θ is highly expressed in skeletal muscle (Avignon et al. 1996). In humans, PKC θ activity and distribution is increased in skeletal muscle of obese diabetic compared to obese normoglycemic humans (Itani et al. 2001). In addition PKC θ mRNA is increased in T2DM patients and inversely correlated with insulin sensitivity (Gray et al. 2003). In these studies, all other PKC isoforms were unaltered. In animals models of T2DM, PKC- δ and - θ phosphorylation is reduced in diabetic Goto-Kakizaki (GK) rats and obese *ob/ob* mice (Avignon et al. 1996), whereas PKC- ϵ , - δ and - θ phosphorylation is increased in the high fat-fed rat model of insulin resistance (Schmitz-Peiffer et al. 1997). Ablation of PKC θ in mice prevents against high fat diet-induced insulin resistance (Kim et al. 2004). The cause of aberrant PKC activation in the development of insulin resistance associated with T2DM is poorly defined. Recent evidence suggests that changes in PKC isoform specific activation can occur in response to increased glucose and/or lipid availability, whereas chronic changes could occur in response to increased glucose and/or insulin concentrations (Schmitz-Peiffer 2000). Thus little is known about the involvement of PKC in insulin signaling to glucose transport in T2DM. Moreover, the distribution and activation of PKC isoforms and the role of these targets on intracellular events in skeletal muscle as related to T2DM is largely unknown. Nevertheless, activation of PKC is likely to be important in the development of diabetic complications (Way et al. 2001).

Defects in MAPK signaling

The effect of T2DM on MAPK signaling in skeletal muscle is incompletely resolved. Activation and expression of p38-MAPK and ERK1/2 in diabetic insulin

sensitive tissues is either aberrant (Koistinen et al. 2003) or unaltered (Krook et al. 2000). In contrast JNK seems to play a key role in the pathogenesis of insulin resistance. JNK is abnormally elevated in various tissues under diabetic conditions (Hirosumi et al. 2002). Moreover JNK knock out mice are protected from obesity-induced insulin resistance (Hirosumi et al. 2002). Therefore JNK inhibition has been proposed as a therapeutic target for the treatment of insulin resistance (Bogoyevitch et al. 2004). Thus little is known of the physiological implications of MAPK regulation in the context of insulin resistant states such as diabetes and obesity.

Glucose-Induced Insulin Resistance

Chronic hyperglycemia is a cardinal feature of diabetes and obesity. Elevation of plasma glucose concentration for 24 hrs in human (Yki-Jarvinen et al. 1987) and 72 hrs in rats (Hager et al. 1991), to pathophysiologically relevant glucose concentrations (10-40 mM) markedly suppresses whole body insulin-stimulated glucose uptake. In addition, selective correction of hyperglycemia normalizes insulin sensitivity (Rossetti et al. 1987), providing compelling evidence that hyperglycemia directly causes insulin resistance.

The mechanism by which hyperglycemia decreases whole body glucose uptake is largely localized to skeletal muscle tissue, and can be explained by reduced muscle glucose utilization and metabolism, particularly glycogen biosynthesis (Yki-Jarvinen et al. 1990). The hyperglycemia-induced impairments in insulin action on skeletal muscle glucose utilization are mediated by defects in glucose transport (Rossetti et al. 1987) and reduced plasma membrane GLUT4 transporter number (Dimitrakoudis et al. 1992). Hyperglycemia-induced defects at different steps of the insulin signaling pathway to glucose transport have also been identified.

Hyperglycemia-induced impairments in PI3K signaling

Hyperglycemia appears to impair the insulin signaling step between PI3K and PKB activation. Isolated EDL muscle incubated for 4-hr with 20 mM glucose exhibit reduced insulin-stimulated glucose uptake and metabolism. In addition insulin-stimulated PKB activation is impaired whereas PI3K and MAPK activities are unchanged (Kurowski et al. 1999). In contrast, post-receptor insulin signaling is increased at the level of IR, IRS-1 and PI3K in parallel with impaired PKB activation in soleus muscle from streptozotocin-injected rats (Oku et al. 2001). Amelioration of glycemia in these rats normalizes PKB activity. Similarly correction of hyperglycemia in the non obese diabetic GK rat normalizes PKB activation and glucose transport (Song et al. 1999) suggesting that impaired PKB activation underlies glucose-induced insulin resistance in skeletal muscle. Interestingly, the toxic effects of glucose are prevented by adding AICAR to the media (Tomas et al. 2002).

Lipid-Induced Insulin Resistance

Management of dyslipidemia is of equal importance to control of hyperglycemia in the care of patients with T2DM. Hyperlipidemia *per se* is an independent primary cause of insulin resistance. Healthy volunteers subjected to

artificial elevation of plasma free fatty acid (FFA) or triglyceride (TG) develop whole body insulin resistance after 4-hr of intralipid infusion (Boden et al. 1995; Roden et al. 1996; Brechtel et al. 2001) and, 2-hr later, both oxidative glucose disposal and muscle glycogen synthesis is diminished. High fat feeding also leads to impaired glucose transport (Grundleger et al. 1982), as well as defects in GLUT4 recruitment to the plasma membrane (Zierath et al. 1997) and expression, in very high fat diets (Leturque et al. 1991, Kahn et al. 1993). Several studies have investigated alterations in insulin signaling in high fat-fed rodents. Insulin resistance has been observed together with diminished IRS-1 tyrosine phosphorylation (Zierath et al. 1997; Anai et al. 1999), PKB and PKC ζ activation (Tremblay et al. 2001; Kim et al. 2002).

Mechanisms of hyperlipidemia-induced insulin resistance

Hyperlipidemia might directly modulate PI3K and MAPK signal transducers activation via lipid intermediates. Long chain fatty acid Coenzyme A, DAG and FFA directly activate PKC (Schmitz-Peiffer 2000). FFA also activate JNK (Gao et al. 2004), whereas ceramide specifically interacts with PKB (Schmitz-Peiffer et al. 1999). FFA activation of PKC θ provides a mechanism for FFA-induced insulin resistance (Griffin et al. 1999) via serine phosphorylation (Li et al. 2004) and degradation of IRS-1 (Gao et al. 2004). FFA activation of JNK promotes insulin resistance via association with and phosphorylation of, IRS-1 on serine 307 (Aguirre et al. 2000) which blocks interaction with the IR and inhibits insulin action (Aguirre et al. 2002). Thus, nutrient oversupply can contribute to diminished insulin signaling at early and intermediate steps of the PI3K signaling pathway. These effects may be mediated by aberrant PKC activation, following intracellular accumulation of glucose and lipid intermediates. Prevention of intracellular accumulation of these intermediates might improve skeletal muscle insulin sensitivity.

Strategies to prevent skeletal muscle insulin resistance

Skeletal muscle insulin resistance is an important pathophysiological feature of T2DM and therefore a major site of action for therapeutic strategies. One approach is to directly modulate, or bypass defective insulin signaling, with the ultimate goal to increase GLUT4 translocation to the plasma membrane and glucose transport. To determine whether these molecules are potential sites of pharmacological intervention to overcome skeletal muscle insulin resistance mechanism of action requires validation. Understanding the molecular mechanisms underlying defective insulin signaling and exercise/stress signaling in genetically or environmentally-induced insulin resistant animal models may prove valuable to the biological validation of diabetes prevention targets.

AIMS

The primary aim of this thesis was to investigate the activation of intracellular signaling pathways following insulin-dependent and -independent stimuli in skeletal muscle from insulin resistant diabetic and/or obese rodents. Defects in insulin-stimulated PI3K and MAPK activation will be further explored in parallel with MAPK and AMPK responses to muscle contraction and stress. AMPK is hypothesized to be a potential therapeutic target for the treatment of insulin resistance and T2DM. Thus the role of the muscle specific AMPK γ 3-subunit in regulating glucose homeostasis and preventing diet-induced insulin-resistance will be determined using AMPK γ 3 transgenic and knock out mice.

This thesis will address the following questions:

- Does acute hyperglycemia lead to skeletal muscle insulin resistance in Wistar and non obese diabetic Goto-Kakizaki rats?
- Does impaired MAPK signaling contribute to skeletal muscle insulin resistance in obese diabetic *ob/ob* mice?
- What is the effect of insulin-independent stimuli on skeletal muscle MAPK signaling in lean and obese *ob/ob* mice?
- Is AMPK signaling intact in obese diabetic *fa/fa* rats?
- Is the AMPK γ 3-isoform a therapeutic target for the treatment of insulin resistance?

EXPERIMENTAL PROCEDURES

Animal Models of Insulin Resistance Used in This Thesis

The Goto-Kakizaki rat model

The GK rat is a non-obese animal model of T2DM. The model was developed by selective breeding over 35 generations of glucose intolerant Wistar rats (Goto et al. 1976; Goto et al. 1988). GK rat exhibit mild hyperglycemia, glucose intolerance, impaired insulin secretion and excessive hepatic glucose production (Picarel-Blanchot et al. 1996). Moreover decreased hepatic insulin sensitivity and moderate insulin resistance in skeletal muscle and adipose tissue have also been described (Bisbis et al. 1993). The GK rat serves as an ideal model to study diabetes without the contribution of dyslipidemia or obesity.

The ob/ob mouse model

The *ob/ob* mouse is characterized by a spontaneous mutation of the leptin gene which prevents secretion of mature leptin and leads to hyperphagia, reduced energy expenditure, hyperglycemia, hyperinsulinemia, severe glucose intolerance, and early-onset morbid obesity (Mordes et al. 1981; Pelleymounter et al. 1995; Chua et al. 1996). The mutation in the leptin gene occurs in a single base pair (C428T) that results in premature termination of leptin synthesis (Coleman 1978). Leptin administration to *ob/ob* mice normalizes all aspects of the obesity and diabetes syndrome (Halaas et al. 1995).

The Zucker fa/fa rat model

Obese Zucker rats have a spontaneous mutation in the extracellular domain of the leptin receptor and exhibit hyperphagia, dyslipidemia, impaired glucose tolerance, and morbid obesity (Chua et al. 1996). The *fa/fa* mutation observed in Zucker rats is an A880C nucleotide missense mutation resulting in reduced cell surface leptin receptor expression and leptin resistance (Yamashita et al. 1997; Crouse et al. 1998; da Silva et al. 1998).

The AMPK γ 3 knock out (Prkag3^{-/-}) and transgenic (Tg-Prkag3) mice models

AMPK is a key mediator of exercise-stimulated glucose transport and fatty acid oxidation (Carling 2004). A spontaneous missense mutation in AMPK γ 3 subunit resulting in the substitution of arginine 225 by glutamine (R225Q) was identified in Hampshire pigs, and shown to be associated with increased skeletal muscle glycogen content (Milan et al. 2000). This suggests that AMPK γ 3 might play a role in regulating glucose homeostasis. Transgenic mice specifically overexpressing wild type (Tg-Prkag3^{wt}) or R225Q mutated (Tg-Prkag3^{225Q}) forms of AMPK γ 3 in white muscle, as well as AMPK γ 3 knock out mice (Prkag3^{-/-}) were generated using the classical targeted mutagenesis technology. Prkag3^{-/-}, Tg-Prkag3^{wt} and Tg-Prkag3^{225Q} mice were phenotyped for the metabolic consequences of genetic modification of AMPK γ 3 expression in skeletal muscle.

Environmentally-induced insulin resistance: high fat feeding

Insulin resistance can be rapidly induced in control rats and mice fed a high fat diet for a short period of time (Storlien et al. 1986, Hedekov et al. 1992, Zierath et al. 1994). Combined euglycemic-hyperinsulinemic clamp and tracer studies reveal that high fat diet-induced insulin resistance first occurs in the liver followed by widespread impairment in insulin action in skeletal muscle and adipose tissues. High fat-fed rat exhibit hyperphagia, reduced energy expenditure, increased adiposity, glucose intolerance, hyperglycemia, hyperinsulinemia and dyslipidemia (Kraegen et al. 1986; Storlien et al. 1993). High fat diet-induced insulin resistance is a flexible approach that allows studying progressive development of the metabolic syndrome (Storlien et al. 1996). The degree of the metabolic defect is proportional to the duration of the diet. In addition, the percentage of fat in the diet also influences the degree of the metabolic defect. AMPK transgenic and knockout mice were placed on a high-fat diet as described below.

Animal Care

GK rats (200-250 g) were purchased from the Department of Endocrinology, Karolinska Hospital (Stockholm, Sweden). Wistar control rats, C57/Bl6 control mice and *ob/ob* mice (12-16 weeks old) were purchased from B&K Universal AB (Sollentuna, Sweden). Zucker (*fa/fa*) rats and lean littermates (11-12 weeks) were purchased from Charles River (Uppsala, Sweden). Transgenic and knock-out AMPK γ 3 mice (8-16 weeks old) were generated as described in paper IV by the Department of Animal Breeding and Genetics, Uppsala Biomedical Center (Uppsala, Sweden). Mice genotyping was performed on tail biopsies from 3 week-old transgenic and knock-out animals. DNA was first extracted using a DNA extraction kit (Qiagen, Hilden, Germany), then amplified by PCR using the primer sequences in table 1, and finally identified on a 4% agarose gel using a DNA ladder (Fermentas GmbH, St. Leon-Rot, Germany).

Table 1. AMPK primer sequences

PRIMERS	AMPK γ 3 KNOCK OUT	AMPK γ 3 OVEREXPRESSOR
Forward	TGGTTGGTGCTCTTTCAGAGACCCAG	AAGATGGCTTGGGTGTGAGGAC
Forward	TTGGCAAATGGACAAATCTGGAGCTAGG	GCTGCCAGCAAACCTAAAC
Reverse	GCTGCTAAAGCGCATGCTCCAGAC	TGCTCCGATTGATCAGTTCC

Rodents were matched for age, sex and body weight. All animals were housed under a temperature- and light- controlled environment and had free access to water and either standard chow or 55% fat (Harlan Teklad, Madison, WI, USA) rodent diets. The high fat diet contained 68% saturated fatty acids (oleic, linoleic and linolenic acid) and 32% unsaturated fatty acids (palmitic and stearic acid). Fasted animals were deprived of chow for 15- to 18-hr (overnight) before the experiment. The Stockholm North Animal Ethical Committee approved all protocols.

Anesthesia and Tissue Sampling

Rats undergoing surgeries for systemic infusion were anesthetized with 125 mg/100g body weight (bw) of ketamine. The day of the *in vitro* experiment animals were anesthetized with either 60 mg/kg bw of sodium pentobarbital (rat) or 0.02 ml/g bw of 2.5% Avertin (mouse).

In vivo glucose infusion

Rat hind-limb muscles were removed immediately after infusion and stored at -80°C for later analysis.

In vitro muscle incubation

Extensor Digitorum Longus (EDL), epitrochlearis and soleus muscle were dissected from the animal, keeping the proximal and distal tendons intact for *in vitro* muscle incubation. Prior to incubation, the epitrochlearis muscle was placed on filter paper moistened with Krebs-Henseleit Buffer (KHB) and excess tissue was removed (Wallberg-Henriksson et al. 1987). Brain, diaphragm, gastrocnemius, heart, liver, quadriceps and white adipose tissue were frozen in liquid nitrogen immediately after isolation for biochemical analysis, determination of protein expression and activation. Blood sample were collected from the tail vein using heparinized microcapillaries (Drummond Scientific Co., USA), centrifuged for 20 min at 2,000 g for plasma sampling and stored at -80°C for later analysis.

IN VIVO METHODS

Hyperglycemic Infusion

The *in vivo* effect of a 3-hr high glucose infusion on insulin signaling was assessed using a hyperglycemic infusion protocol (paper I). A catheter was placed in the jugular vein of GK and Wistar rats for systemic infusion. Animals were used for experiment 4 days after surgery and were studied under euglycemic (glucose levels at ~5 mM) or hyperglycemic (glucose levels maintained at ~20 mM) conditions, in the absence or presence of insulin. For all experimental conditions, endogenous insulin secretion was suppressed by a constant infusion of somatostatin (2 µg/kg.min). Sixty minutes after the onset of somatostatin infusion, animals received either saline (euglycemic) or a bolus of glucose (0.5 ml of 30% glucose), followed by continuous glucose infusion to raise blood glucose concentration to approximately 20 mM (hyperglycemic). Three hours thereafter, animals were either sacrificed or administered a bolus of insulin (20 mU, Actrapid, Novo Nordisk, Bagsvaerd, Denmark), followed by a continuous insulin infusion (3 U/min/kg bw) over a 20-min period. Blood samples for plasma glucose and insulin concentration were collected from the tail vein at different time points during the infusion.

Blood Chemistry

Blood glucose was measured using a One Touch glucose monitor (Lifescan Inc., Milpitas, CA, USA). Plasma insulin was measured using a Radioimmunoassay (Rat Insulin RIA Kit, Lincoln Research Inc., USA) (paper I).

Tolerance Tests

Glucose (2 g/kg bw), insulin (0.75 mU/kg bw) or AICAR (0.25 g/kg bw) was injected intraperitoneally to overnight fasted animals. Blood was sampled from a tail incision before and during the glucose tolerance test. Blood glucose concentration was measured using a One Touch glucose monitor as described above (paper III and IV).

Swimming Exercise Protocol

The effect of exercise on skeletal muscle glycogen content was determined in paper IV. Age and weight matched AMPK γ 3 transgenic and knock-out mice were assigned to sedentary or exercise groups. Six mice swam together in a plastic container (45 cm diameter) {Musi, 2001 #285} filled with water to a depth of 40 cm. Water temperature was maintained at 33-35°C. Mice swam for 4 X 30-min intervals separated by 5-min rest periods. After the last swim interval, mice were dried and either studied immediately or put in their cage for a 2.5-hr recovery period. At the onset of the recovery period, mice received an intraperitoneal glucose injection as described above and were given free access to standard food and water.

***IN VITRO* METHODS**

Muscle Incubation

Incubation media were prepared from a pre-gassed (95% O₂/5% CO₂) stock of KHB containing 5 mM 4-(2-HydroxyEthyl)-1-PiperazineEthaneSulfonic acid (HEPES) supplemented with either 0.1% Bovine Serum Albumine (BSA) (RIA grade) or 3.5% BSA Fatty Acid Free (FAF). Isolated muscles were incubated in either 1 ml (mice) or 2 ml (rats) of media in a shaking water bath. Water temperature was maintained at 30°C. The gas phase in the vial was 95% O₂/5% CO₂. Incubation media contained 5 mM glucose and either 15 mM (papers II, III, IV) or 35 mM (paper I) mannitol. Immediately after dissection and before stimulation, muscles recovered in oxygenated KHB for 15-30-min. Insulin-, AICAR- and PMA-stimulated conditions are explained in detail in each paper.

Hyperglycemic Stimulus

To study the direct effect of hyperglycemia on insulin signaling, the infusion protocol previously described in an *ex vivo* experimental setting was mimicked (paper I). After pre-incubation, skeletal muscles were incubated at 30°C for 3-hr in KHB supplemented with 0.1% BSA and 25 mM glucose. To prevent a shortage of glucose in

the incubation media, muscles were transferred to identical fresh media after 1.5-hr. Thereafter muscles were incubated in the absence or presence of 60 nM insulin for 20-min.

Hypoxic Stimulus

Hypoxic condition is achieved by pre-gassing KHB with 95% N₂/5% CO₂. KHB is then supplemented with 0.1% BSA (RIA grade). Isolated rat muscles were incubated in hypoxic media for 80 min in a shaking water bath (paper III). Water temperature was maintained at 30°C. The gas phase in the vial was 95% N₂/5% CO₂. Muscles were either frozen immediately for later analysis or transferred to oxygenated glucose free media containing 2 mM pyruvate for 15-min. Thereafter, glucose transport activity and AMPK and PI3K activation were measured.

Muscle Contraction Stimulus

The contraction protocol is designed so that muscle undergoes a tetanic isometric contraction event. Following pre-incubation, isolated mouse muscles were placed inside a temperature-controlled (30°C) stimulation chamber and immersed in 4 ml of KHB identical to pre-incubation condition. Each muscle was positioned between two platinum electrodes with the distal tendon mounted to the bottom of the chamber. The proximal tendon was connected to a jeweler's chain, which was fixed to an isometric force transducer (Harvard Apparatus Inc., South Natick, MA, USA). Resting tension was adjusted to 0.25 g for mouse EDL (paper II) or 0.5 g for rat epitrochlearis muscle (paper III). Isometric tension development during the contraction protocol was recorded using a compact 2-Channel Student Oscillograph (Harvard Apparatus Inc.). Isometric muscle contraction was achieved via electrical stimulation. Muscles were stimulated at a frequency of 100 Hz (0.2 ms pulse duration, 10 V amplitude), delivered at a rate of 0.2-s contraction every 2-s for 10-min. Pulses were generated by a Tektronix TM 503 Power Module (Beaverton, OR, USA) and amplified on a 4-Channel Power Amplifier (Somedic, Sollentuna, Sweden). Basal muscles were treated as described above, minus electrical stimulation. Muscles were then either frozen immediately for biochemical analysis, protein expression and activation measurements or further incubated for the assessment of metabolic readouts.

Glucose Transport

After pre-incubation, muscles were incubated at 30°C for 10-min in glucose-free KHB supplemented with 0.1% BSA and 20 mM mannitol to rinse glucose from the extracellular space (papers III, IV). The rate of glucose transport is linear between 5- and 120-min in rat epitrochlearis muscle (Hansen et al. 1995). Thereafter, glucose transport activity was determined using 2-deoxy-[1,2,³H]-glucose (2.5 μCi/ml). Extracellular space was measured using [¹⁴C]-mannitol (0.7 μCi/ml). Muscles samples were dissolved in 0.5 N NaOH and counted for [³H] and [¹⁴C] activity by liquid scintillation. Intracellular glucose accumulation was assessed by dual label calculation as described (Wallberg-Henriksson et al. 1987).

Oleate Oxidation

Muscles were pre-incubated at 30°C in the presence of insulin with or without AICAR for 20-min in KHB supplemented with 3.5% BSA-FAF and 10 mM glucose (paper IV). Thereafter, muscles were incubated in identical medium containing [1-¹⁴C]-oleate (0.4 μCi/ml) for 1-hr. The medium was acidified by 0.5 ml of 15% Δ'-pyrroline-5-carboxylic acid, and liberated CO₂ was collected in center wells containing 0.2 ml of Protosol for 1-hr. Center wells were removed and counted for [¹⁴C] activity by liquid scintillation.

Biochemical Analysis

Gastrocnemius muscle was removed from anesthetized animal as mentioned earlier. Glycogen was determined fluorometrically on muscle HCl extracts, as described previously (Lowery and Passonneau 1972). For TG measurements, skeletal muscle was homogenized in a heptan:isopropanol 3:2, Tween 1% mixture and removed of free glycerol. Thereafter, skeletal muscle TG were measured by a colorimetric assay with a TG/glycerol blanked kit (Roche Applied Science, Paris, France) using SeronormTM lipid as standard.

Tissue Homogenization

Mouse or rat tissues were homogenized on ice in homogenization buffer, as described in each paper. Protein was determined on homogenates using a commercially available kit based on the Bradford method (Bio-Rad Laboratories Inc., Hercules, CA, USA).

Protein and Lipid Kinase Activity Measurement

Following protein determination, aliquots of muscle or cell homogenates were immunoprecipitated with the appropriate antibody previously equilibrated with either protein A sepharose (PI3K assay), protein G sepharose (AMPK assay) or protein A/G sepharose mix (PDK-1 and PKC-ζ assay). Immunoprecipitates were washed in buffer, as described in each paper. Thereafter protein kinase activity was determined in the presence of the kinase substrate and coactivator when needed, and [γ-³²P]-ATP (table 1). For PI3K activity measurement, the radioactive lipid product was identified by thin layer chromatography and quantified by autoradiography. For protein kinase activity determination, the radioactive peptide product was spotted on phosphocellulose paper (P81) and radioactivity was assessed by liquid scintillation counting. Table 2 presents the characteristics of the antibodies used for immunoprecipitation.

Table 2. Protein Kinase Assay Reaction Conditions

PROTEIN KINASE		SUBSTRATE	Coactiv.	REACTION CONDITIONS	PRODUCT
AMPK	cell	LKKLTLRPSFSAQ (ADR1)	AMP	10 min, T _{room}	³² P-ADR1
	muscle	HMRSAMSGHLVKRR	AMP	60 min, 30°C	³² P-SAMS
PDK-1	muscle	KTFCGTPEYLAPEVRREPRILSEE EQEMFRDFDYIADWC (PDK-tide)	-	10 min, 30°C	³² P-PDKtide
PI3K	muscle	L- α -phosphatidylinositol (PI)	-	20 min, T _{room}	PI- ³² P ₃
PKC ζ	muscle	ERM RP RK R Q G S V R R R V	PS	20 min, T _{room}	³² P-peptide

Western Blot Analysis

Following protein determination, aliquots of tissue homogenates were suspended in the Laemmli sample buffer (Laemmli 1970). Equal amounts of protein were separated by sodiumdodecylsulfate polyacrylamide gel electrophoresis and transferred to polyvinylidenedifluoride membranes. Thereafter the membrane was blocked with 7.5% non-fat milk for 2-3-hr at room temperature and incubated with primary antibody (table 2) overnight at 4 °C. The membrane was then washed with Tris-Buffered Saline Tween (TBST) (10 mM Tris, 140 mM NaCl, 0.02% Tween, pH 7.6) and incubated with appropriate secondary antibody for 1-hr at room temperature. After an additional washing with TBST, the proteins of interest were visualized by enhanced chemiluminescence (ECL or ECL+, Amersham Biosciences, Buckinghamshire, UK) and subsequent autoradiograph. The corresponding bands were quantified by densitometry (Molecular Analyst Software). Table 2 presents the characteristics of the antibodies used for Western Blot analysis.

RNA Extraction and cDNA Synthesis

Skeletal muscle RNA was extracted using Trizol reagent (Sigma) and purified with isopropanol and ethanol. Thereafter purified RNA was treated with DNase I using DNA-free kit (Ambion, Huntingdon, UK) according to Ambion's protocol. DNase-treated RNA then served as template for cDNA synthesis using SuperScript First Strand Synthesis System (Invitrogen, Stockholm, Sweden) and appropriate oligo(dT) primers.

Quantitative PCR

mRNA quantification was performed using real-time PCR with the ABI PRISM 7700 Sequence Detector System (Applied Biosystems, Warrington, UK) and SYBR-green. The relative quantities of target transcripts were calculated from duplicate samples after normalization of the data against housekeeping gene 36B4 (acidic ribosomal phosphoprotein). Primers were selected using PRIMER EXPRESS (Applied Biosystems). Transcript sequences were obtained from ENSEMBL and GENBANK databases.

Table 3. Antibody Characteristics

ENZYME		EPITOPE	MW (kDa)	SOURCE
ACC	P-ser 79	rat aa 73-85	257	Upst. Biotech., Lake Placid, NY
	ACC β expr.	hum. aa 1501-1638; C-terminal	257-280	Upst. Biotech.
AMPK	P-thr 172	hum. α Synthetic Peptide (SP)	62	Cell Sign. Tech., Beverly, MA
	IP anti- α 1 expr.	rat α 1 and α 2 hum. aa 376-392	- 63	Gift from Arexis, Sweden Upst. Biotech.
ERK	P-tyr 204/ P-thr 202 expr.	hum. aa 196-209	44/42	New Engl. Biolab., Boston, MA
		rat aa 219-358	44/42	Transd. Lab., Lexington, KY
JNK	P-thr 183/ P-tyr 185 expr.	synth. phospho-peptide	46/54	Cell Sign. Tech.
		hum. JNK2	46/54	Cell Sign. Tech.
p38	P-thr 180/ P-tyr 182 expr.	rat SP	43	Cell Sign. Tech.
		hum. SP	43	NEB
PDK-1	P-thr 373/376 P-ser 241 expr.	hum. SP	60-68	Cell Sign. Tech.
		hum. SP	63	Cell Sign. Tech.
		hum. C-terminal	58-68	Cell Sign. Tech.
PKB	P-ser 473 expr.	mouse SP	62	NEB
		mouse SP	62	NEB
PKC α/β	P-thr 638/641 α expr. β expr.	hum. α SP	82/80	Cell Sign. Tech.
		hum. aa 270-427; ATP BD	82	BD Biosciences, CA
		hum. aa 126-324; Ca ⁺⁺ BD	80	BD Biosciences
PKC δ	P-ser 643 expr.	human SP	78	Transd. Lab.
		hum. aa 114-289; Ca ⁺⁺ BD	78	Cell Sign. Tech.
PKC θ	P-thr 538 expr.	hum. SP	79	Cell Sign. Tech.
		hum. aa 21-217; Ca ⁺⁺ BD	79	Transd. Lab.
PKC ζ	P-thr 403/410 IP expr.	hum. SP	76	Cell Sign. Tech.
		rat C-terminal aa 577-592	-	Upst. Biotech.
		hum. PKC ζ ; substrate BD	72	Transd. Lab.
PI3K	P-tyr IP	hum. SP	-	Transd. Lab.

BD = binding domain;

SP = synthetic peptide designed to react with residues surrounding the sites of interest.

expr. = protein expression

Table 4. Primer Sequence

GENE	DATABASE ID	PRIMER	
		FORWARD	REVERSE
LPL	ENSMUST00000015715	CTGGGCTATGAGATCAACAAGGT	AGGGCATCTGAGAGCGAGTCT
CD36	ENSMUST00000003024	GCCAAGCTATTGCGACATGA	AAAAGAATCTCAATGTCCGAGACTTT
CPT1	ENSMUST00000023287	ACCACATCCGCAAGCA	TTCCTCAGCTGTCTGTCTTGGGA
UCP3	ENSMUST00000032958	GCCAGGGAGGAAGGAGTCA	TGACAATGGCATTCTTGTGATG
Cit. Synth.	ENSMUST00000005826	GCAAATCAGGAGGTGCTTGTCT	TCTGACACGTCTTTGCCAACTT
Cytochr. C	NM007808	GGAAAAGGGAGGCAAGCATAA	GCAGCCTGGCCTGTCTTC
HAD	ENSMUST00000029610	TGGACGGGTGGCATGAA	TGGAAGGACTGGGCTGAAAT

Statistics

Data are represented as mean±SE. Differences between two groups were determined by unpaired Student's *t*-test. Differences between more than two groups were determined by one-way Analysis of Variance (ANOVA) followed by the Fisher's least significant difference *post hoc* analysis. Significance was accepted at $P < 0.05$.

RESULTS and DISCUSSION

GK Rats are Hyperglycemic and Insulin Resistant

GK rats are a non-obese model of T2DM. They exhibit mild hyperglycemia (Song et al. 1999 and paper I) and glucose intolerance (Krook et al. 1997). In addition they display skeletal muscle insulin resistance at the level of glucose transport (Krook et al. 1997) and early and intermediate steps of the PI3K signaling cascade (Krook et al. 1997 and paper I). These defects are functional and fiber-type specific (Song et al. 1999).

GK rats are a useful model to study the toxic effects of glucose on muscle intracellular signaling. Indeed restoration of glycemia with phlorizin (Krook et al. 1997) or thiazolidinedione (Kano et al. 2001) normalizes signaling defects at intermediate steps of PI3K signaling pathway, suggesting that glycemia modulates insulin intracellular signaling. In paper I, the question of whether an acute elevation of glycemia would normalize or further impair insulin signaling to glucose transport in skeletal muscle from diabetic GK rats was addressed.

Acute Normalization of Glycemia Does Not Improve PI3K Signaling in GK Rats

Chronic hyperglycemia is a characteristic feature of insulin resistance and T2DM. Glucose itself can impair insulin-stimulated PI3K signaling, and this is referred to as “glucose toxicity”. Mildly hyperglycemic GK rats exhibit impaired insulin action at the level of PI3K and PKB (Krook et al. 1997, Song et al. 1999 and paper I). These defects are functional, since protein expression is not affected (Krook et al. 1997, Song et al. 1999 and paper I). Normalization of glycemia results in normalization of insulin signaling at the level of PKB (Krook et al. 1997, Song et al. 1999, Oku et al. 2001), whereas the PI3K defect persists. Thus, PKB, rather than PI3K, appears to be sensitive to the level of glycemia. To test when hyperglycemia-induced defects at the level of PKB can occur acutely in skeletal muscle, Wistar rats were infused with 20 mM glucose for 3 hrs. Insulin-stimulated PI3K, PKB and ERK1/2 activation was unaltered by hyperglycemia under these conditions. Thus, a more prolonged period of hyperglycemia may be needed to impair PI3K signaling in normoglycemic rats rendered hyperglycemic. This hypothesis is consistent with *in vivo* observations, whereby hyperglycemic (streptozotocin-injected) 10 week-old rats exhibit altered insulin-stimulated PKB activity (Oku et al. 2001). In contrast, *in vitro* observations provide evidence to suggest that 4 hrs seem to be sufficient to impair PKB activation (Kurowski et al. 1999). In both cases, appropriate PI3K action is retained.

We hypothesized that impaired insulin signaling in diabetic GK rats would be improved after acute normalization of glycemia, yet these signaling defects were evident, regardless of the level of glycemia (paper I). Interestingly, basal responses for PI3K and PKB were further reduced in GK rats, although protein expression was unaltered. Thus a more prolonged period of euglycemia in GK rats is also likely to be necessary to achieve improvements in insulin signaling. The mechanism by which hyperglycemia induces defects in PI3K signaling may involve intracellular accumulation of glucose metabolites, such as glucosamine (Parker et al., 2003),

impairments in serine kinases, or altered phosphatase activity (Filippis et al. 1997; Marques et al. 2000). Thus a 3-hr elevation of glycemia is insufficient to induce an impairment in insulin signaling at the level of PI3K and/or PKB.

Acute Hyperglycemia Differentially Modulates PKB and PKC ζ

The possibility of a differential effect of glucose on parallel signal transduction pathways, such as PKB, PKC ζ and ERK1/2, was evaluated. Basal PKC ζ activity was elevated under hyperglycemic conditions in Wistar and GK rats, whereas ERK1/2 phosphorylation was unchanged in either animal model (paper I). To determine whether the glucose-induced effect on PKC ζ is direct, isolated skeletal muscle was exposed to 5 or 25 mM glucose *in vitro*. Consistent with our *in vivo* observation, PKC ζ activity and phosphorylation was increased in skeletal muscle exposed to 25 mM glucose (paper I). This observation is supported by earlier studies, whereby exposure of isolated skeletal muscle (Kawano et al. 1999) or mesangial cells (Kikkawa et al. 1994) to high extracellular concentrations of glucose was associated with PKC ζ translocation. Interestingly normalization of glycemia in diabetic animals corrects defective PKC ζ activation (Kanoh et al. 2000, Kanoh et al., 2001), suggesting that in addition to PKB, PKC ζ is also modulated by the level of glycemia. Nevertheless PKC ζ activation appears to be altered more rapidly than PKB.

The mechanism by which hyperglycemia induces PKC ζ activation independently of PIP₃ is currently unknown, but might involve another acidic lipid, namely phosphatidic acid (PA). Indeed glucose has been reported to directly activate PKC ζ through a sequential activation of the dantrolene-sensitive, non-receptor proline-rich tyrosine kinase-2 and phospholipase D (Bandyopadhyay et al. 2001). Activation of PLD results in intracellular accumulation of PA. Thus glucose may selectively activate PKC ζ through a PI3K-independent mechanism involving PA.

Glucose Increases Conventional and Novel PKC Activity

To test whether glucose effects on PKC ζ are isoform-specific, conventional and novel PKC activation was assessed after acute exposure of isolated skeletal muscle to 5 or 25 mM glucose *in vitro*. An increase in PKC- α/β and - δ but not - θ phosphorylation was noted (paper I). This is consistent with a previous study, whereby glucose was reported to activate several PKC isoforms including PKC- α , - δ , - ε and - ζ in Rat1 fibroblasts (Berti et al. 1994). PKC activation may account for glucose-induced insulin resistance (Kroder et al. 1996) through a glucosamine mediated mechanism (Filippis et al. 1997). Thus the acute effects of hyperglycemia on PKC ζ are unspecific to this isoform.

Glucose Positively Modulates PDK-1

PKB, PKC and ERK are downstream substrates of PDK-1 and in that regard belong to the AGC kinases superfamily [comprising the prototypes protein kinase A (PKA), G (PKG), and C (PKC)]. To further delineate the differential effect of glucose on activation of these AGC kinases, glucose effects on upstream PDK-1 were determined. In isolated soleus muscle exposed to 25 mM glucose for 3 hrs, PDK-1 activity and tyrosine phosphorylation was increased 1.6-and 2-fold, respectively,

regardless of whether insulin was absent or present (paper I). Activation of PDK-1 by glucose provides a potential mechanism for the observed glucose-mediated changes in PKC activity. However glucose did not alter PKB or ERK1/2 phosphorylation indicating a divergence in the effects of PDK-1 on its downstream AGC substrates. Differences in PDK-1 intracellular localization following glucose exposure may provide a mechanism for the divergent effects on PKB and PKC ζ . Indeed studies in 3T3L1 adipocytes overexpressing wild type or plasma membrane targeted PDK-1 show that full activation of PKB requires PDK-1 translocation to the plasma membrane, whereas PKC ζ activation can be activated by cytosolic PDK-1 (Egawa et al. 2002).

Table 5. Glucose and insulin effects on PDK-1 activity and tyrosine and serine phosphorylation

PDK-1	activity	P-tyrosine	P-serine
insulin	↔	↑	shift
glucose	↑	↑	↑?
glucose + insulin	↑	additive	shift

Glucose-induced activation of PDK-1 appears to involve phosphorylation on tyrosine and serine residues, consistent with previously published observations (Casamayor et al. 1999; Park et al. 2001). In our experimental approach, insulin does not alter PDK-1 activity, despite increased tyrosine phosphorylation of the enzyme (table 5). Conversely, insulin was shown to induce a concomitant increase in tyrosine phosphorylation, activity and PDK-1 translocation to the plasma membrane in HEK293 cells transfected with PDK-1 (Park et al. 2001). Thus in our model, tyrosine phosphorylation of PDK-1 may be necessary, but insufficient for activation of the enzyme. In addition the observation that PDK-1 activation occurs independently of PIP₃ supports the dispensability of PIP₃-mediated plasma membrane relocation.

Comparative Simultaneous Effect of Insulin on MAPK Signaling

In addition to PI3K signaling, insulin also turns on MAPK signaling. Thus, simultaneous activation of p38-MAPK, ERK1/2 and JNK by insulin was assessed by detailed time course and dose-response studies. Insulin induced a robust activation of all three MAPK in a similar time- and dose-dependent manner in soleus and EDL muscle. Half maximal phosphorylation was reached within 4 min, whereas maximal effects were noted after 20 min of insulin exposure. Moreover MAPK phosphorylation in response to insulin was maximal when insulin concentration reached 120 nM (paper II). A previous *in vivo* study provides evidence that the time course for insulin-induced activation of the three MAPK is distinctly different, with activation of JNK occurring within seconds, p38-MAPK within 2 min, and ERK1/2 occurring within 4 min (Moxham et al. 1996). Thus *in vitro* insulin activation of MAPK seems to take longer time than *in vivo*. This might be due to insulin-induced hemodynamic effects that render the hormone more effective in activating MAPK when in the systemic circulation. Nevertheless simultaneous *in vitro* activation of all three MAPK modules raises the question of specificity in signal transduction. MAPK are known to have both distinct and identical substrates (Chen et al. 2001), thereby

providing a mechanism for specific signaling as well as amplification of the response. This might be of particular importance in disease states.

One interesting observation is that insulin-stimulated ERK1/2 phosphorylation appears to be biphasic in EDL. This suggests that at least two distinct activating mechanisms may account for insulin-stimulated ERK1/2 phosphorylation. Recent evidence shows that the divergence occurs at the level of MEK, the upstream activator of ERK1/2. Indeed wortmanin -sensitive and -insensitive ERK1/2-activating pathways have been identified in a perfused rat hind limb model (Wojtaszewski et al. 1999). Wortmanin-insensitive activation of ERK1/2 signaling appears to be PKC-dependent (Nakamura et al. 1996), whereas wortmanin-sensitive ERK1/2 activation in muscle is PI3K-dependent. Thus insulin activation of ERK1/2 might recruit two distinct signaling mechanisms upstream of MEK mediated by PKC and PI3K, respectively and this might account for the observed biphasic-like insulin-stimulated ERK1/2 phosphorylation.

Fiber-Type Specific MAPK Signaling

Recent evidence shows that insulin activation of PI3K signaling is fiber-type specific (Song et al. 1999). To determine whether MAPK signaling also occurs in a fiber-type specific manner maximal (120 nM for 20 min) insulin effects on MAPK phosphorylation in soleus and EDL muscle were compared. Insulin action on p38-MAPK was more transient and less robust in oxidative versus glycolytic muscle, whereas ERK1/2 response to insulin was unchanged. Interestingly JNK protein expression was higher in glycolytic versus oxidative muscle, whereas p38-MAPK and ERK1/2 protein expression was similar (paper II). This observation is counter intuitive, since slow-twitch oxidative fibers are generally considered to be highly sensitive to stimulation by insulin. However contraction induced p38-MAPK activation is reportedly increased in fast-twitch muscle, whereas ERK1/2 activation is similar between slow- and fast-twitch muscle fibers (Wretman et al. 2000).

Effect of Different Stimuli on MAPK Signaling

MAPK can be activated by different stimuli including insulin, contraction and PMA, a DAG analog. MAPK activation appears to require activation of specific MEKK upstream kinases to ensure specificity of the signal (Chen et al. 2001). However upstream MEKK activating mechanisms are uncertain. In paper II, the additive effects of insulin, contraction and PMA on MAPK phosphorylation was determined. Insulin and PMA elicited an additive response on JNK and ERK1 phosphorylation, whereas insulin and contraction did not elicit additive effects on any of the MAPK studied. Interestingly the combined effect of insulin and contraction on p38-MAPK phosphorylation was blunted (paper II). This is consistent with previous reports of reduced insulin action on PI3K in exercised skeletal muscle (Goodyear et al. 1995, Wojtaszewski et al., 1997). Although the effect of prior insulin exposure on contraction-stimulated MAPK activation was not assessed, one could speculate that during the initial phases of skeletal muscle contraction, the energy supply for intracellular signaling is turned on, whereas processes involved in energy storage are turned off. Since insulin elicits a storing signal and the contracting muscle needs energy, the skeletal muscle may become temporarily insulin resistant.

***Ob/ob* mice are Insulin Resistant**

Insulin resistance in *ob/ob* mice is rather well-defined and partly mirrors the defects described in obese diabetic patients. Impaired insulin signaling in this animal model is associated with reduced IR number and activation (Kahn et al. 1973). The effect of the remaining insulin signaling through IR on insulin-stimulated MAPK activation was determined in skeletal muscle from obese insulin resistant *ob/ob* mice. Insulin-stimulated ERK1/2 and JNK phosphorylation was reduced, whereas absolute p38-MAPK activation was unchanged. These defects are functional since ERK1/2 and JNK protein expression was intact (paper II). Insulin activation of ERK1/2 is also impaired in muscle from obese diabetic Zucker rats (Osman et al. 2001). This suggests that insulin activation of ERK1/2 and JNK may be mediated by IR/IRS-1 signaling. In contrast, p38-MAPK protein expression was reduced in parallel with increased basal phosphorylation, consistent with a previous observation in skeletal muscle from T2DM patients (Koistinen et al. 2003). Furthermore basal ERK1 in EDL (paper II) and JNK phosphorylation in soleus (paper II) tended to be elevated (non significant), consistent with observations in adipocytes from T2DM subjects (Carlson et al. 2003). Normalization of basal p38-MAPK phosphorylation prevented the insulin-stimulated decrease in GLUT4 protein levels (Carlson et al. 2003), suggesting that aberrant p38-MAPK activation contributes to the pathogenesis of insulin resistance. Thus insulin-stimulated activation of all three MAPK is impaired in muscle from obese insulin resistant mice, whereas basal p38-MAPK phosphorylation is increased.

Contraction Effects on ERK1/2 and JNK Activation is Intact in *ob/ob* Mice

Defects in insulin-stimulated PI3K (table 6) and MAPK signaling (paper II) contribute to skeletal muscle insulin resistance in *ob/ob* mice. Moreover, contraction- and hypoxia-stimulated glucose transport is preserved in insulin resistant obese *fa/fa* rat (paper III). To determine whether insulin-independent MAPK activation is altered or preserved in insulin resistant *ob/ob* mice, isolated EDL muscle was contracted and/or incubated with PMA. Contraction elicited a robust activation of all three MAPK in lean mice. In addition contraction-stimulated ERK1/2 and JNK phosphorylation was intact in EDL muscle from *ob/ob* mice, whereas p38-MAPK phosphorylation was slightly reduced (non significant) (paper II). This might be due to reduced p38-MAPK protein expression. MAPK have been postulated to mediate exercise-induced improvement in insulin sensitivity, although the underlying mechanism remains largely uncertain. There is evidence supporting that p38-MAPK might directly intervene at the level of GLUT4 activation (Somwar et al. 2001), whereas ERK1/2 appears to be dispensable for exercise-stimulated glucose transport (Wojtaszewski et al. 1999). Thus activation of ERK1/2 and JNK via insulin-independent stimuli such as contraction may bypass defective insulin signaling in insulin resistant obese states.

PMA Effects on ERK1/2 and JNK Activation is Intact in *ob/ob* Mice

PKC isoforms have been suggested to be upstream activators of MAPK following insulin and contraction stimulation (Letiges et al. 2002, Formisano et al., 2000, Chen et al., 2002). Activation of conventional and novel PKC isoforms can be induced by the use of PMA. The effects of PMA on MAPK phosphorylation in *ob/ob*

mouse skeletal muscle were determined. PMA elicited a robust activation of all three MAPK in lean mice. This is consistent with the literature whereby PKC are shown to be upstream activators of all three MAPK (Tsakiridis et al. 2001). In *ob/ob* mice, PMA-induced ERK1/2 phosphorylation was preserved, whereas effects on JNK tended to be reduced (~29%, non significant) (paper II). This divergence in ERK1/2 and JNK phosphorylation may be due to PKC isoform specific activation, since ERK1/2 and JNK protein expression was unaltered. This is consistent with PKC- ϵ isoform-specific MAPK activation in heart (Baines et al., 2002). Altered PKC- α , - ϵ and - θ isoform distribution in skeletal muscle is also associated with an insulin resistance phenotype in Zucker *fa/fa* rats (table 6). Another possibility is that PKC have positive effects on ERK1/2 and negative effects on JNK activation, as shown in rat adipocytes and L6 myotubes incubated in the presence of a PKC inhibitor (Standaert et al. 1999). PMA induced p38-MAPK phosphorylation was totally blunted in *ob/ob* mice in response to PMA, possibly due to the reduction in protein expression (paper II). However the results obtained for contraction-stimulated p38-MAPK phosphorylation suggest that reduced protein expression only partially accounts for blunted PMA effects on p38-MAPK activation and additional upstream regulatory mechanisms might be impaired. This is the first evidence showing that ERK1/2 and JNK signaling are intact following insulin-independent PMA stimulation of EDL muscle from insulin resistant obese mouse model. However caution should be made regarding the role of PKC isoforms, since specific positive and negative involvement of these kinases can play a role in the development of insulin resistance (Kim et al. 2004, Li et al., 2004).

Zucker *fa/fa* Rat are Glucose Intolerant and Insulin Resistant

Rats homozygous for the leptin receptor (*fa*) gene develop severe obesity and a T2DM-like syndrome. The absence of leptin receptor leads to dysregulation of central energy balance, resulting in hyperphagia and subsequent profound central and visceral obesity (Yamashita et al. 1997; Crouse et al. 1998; da Silva et al. 1998). Whole body lipid oversupply causes glucose intolerance and skeletal muscle insulin resistance at the level of glucose transport and PI3K signaling (paper III).

Exercise is an alternate insulin-independent pathway to increase glucose transport and counteract muscle insulin resistance. AMPK is a key mediator of exercise-stimulated glucose transport in skeletal muscle and therefore a potential therapeutic target to combat insulin resistance in T2DM. Isoform specific activation of AMPK was determined in skeletal muscle from obese insulin resistant Zucker *fa/fa* rats to assess whether this pathway is impaired or preserved.

Contraction-Stimulated AMPK α 1 Isoform Specific Defect in *fa/fa* Rat

T2DM and obesity are associated with skeletal muscle insulin resistance at the level of glucose transport (Zierath et al. 1996) and fatty acid oxidation (Kelley et al. 1994). AMPK regulates glucose and lipid metabolism (Carling 2004), by an insulin-independent mechanism. Skeletal muscle expresses AMPK- α 1 and - α 2 catalytic subunits (Stapleton et al. 1996). Thus contraction- and hypoxia-stimulated AMPK α catalytic subunit specific activation was measured in glycolytic muscle of obese insulin resistant Zucker *fa/fa* rats (paper III). Hypoxia and contraction increased AMPK- α 1 and - α 2 activity in lean rats, consistent with previous observations (Mu et al. 2001).

Moreover in Zucker *fa/fa* rats, a contraction-stimulated AMPK α 1-isoform specific defect in glycolytic muscle was observed. In contrast, hypoxia-stimulated AMPK α 1 activation was normal. Thus contraction and hypoxia differentially modulate AMPK α 1-subunit activation in glycolytic *fa/fa* muscle. Furthermore hypoxia had a greater effect on AMPK α 1 activity compared to contraction suggesting that the intensity of the cellular distress determines AMPK α isoform-specific activation. This is consistent with AMPK α 1-subunit being activated by high intensity exercise (Fujii et al. 2000) and might be due to the ATP-depleting effect of hypoxia that is more dramatic than the contraction effect (Fujii et al. 2000). In Zucker *fa/fa* rat (Bergeron et al. 2001) and T2DM patients (Musi et al. 2001), AMPK α -subunit protein expression is unaltered in skeletal muscle.

Basal AMPK α 1-associated activity was reduced in skeletal muscle from Zucker *fa/fa* rats (paper III). This observation is consistent with previous observations in T2DM patients, whereby AMPK α 1 activity tended to be decreased (Musi et al. 2001). AMPK is a stress sensor and stress factors inherent to these experiments – i.e. muscle stretch (Wojtaszewski et al. 2000) - might have revealed an AMPK α 1 isoform-specific defect in glycolytic *fa/fa* muscle. In addition nutrient oversupply in Zucker *fa/fa* rat might differentially regulate AMPK α -subunit specific function (Musi et al. 2001). Since several AMPK upstream kinases are likely, an AMPK α 1 upstream kinase-specific defect in glycolytic muscle of obese insulin resistant Zucker *fa/fa* rat cannot be excluded.

AMPK α 2 activation was normal under both contraction- and hypoxic-stimulatory conditions (paper III). Furthermore AMPK- α 1 and - α 2 isoforms appear to be regulated independently by different stimuli. Since activation of α 2, but not α 1, is associated with a decrease in phosphocreatine:creatinine (P-Cr:Cr) ratio (Fujii et al. 2000), contraction and hypoxia might induce distinct changes in AMP:ATP and P-Cr:Cr ratios that differentially activate AMPK. Thus the intensity of the stimuli and the resulting distinct intracellular stress may determine AMPK α isoform-specific activation. This is consistent with AMPK γ -subunits differing in their AMP sensitivity and muscle fiber type specific AMPK heterotrimer expression (Mahlpuu et al. 2004). Furthermore AMPK α catalytic subunit substrate specificity (Woods et al. 1996) and isoform specific subcellular localization (Salt et al. 1998) may provide additional regulatory mechanisms for AMPK isoform specific activation by distinct stimuli.

Contraction- and Hypoxia-Stimulated Glucose Transport is Intact in *fa/fa* Rats

Contraction- and hypoxia-stimulated glucose uptake was intact in glycolytic muscle from obese Zucker *fa/fa* rats despite insulin resistance (paper III), consistent with previously published observations (Azevedo et al. 1995). Thus the glucose transport effector system is intact in diabetic muscle stimulated with insulin-independent stimuli. Substantial evidence suggests that AMPK is activated during contraction and hypoxia, concurrently with an increase in glucose uptake paper III (Bergeron et al. 1999, Hayashi et al. 2000, Hayashi et al. 1998, Mu et al. 2001). Thus AMPK activation may prove a valuable strategy to bypass obesity-driven skeletal muscle insulin resistance through activation of the glucose transport effector system.

Contraction-stimulated glucose transport is preserved in glycolytic muscle from Zucker *fa/fa* rat despite impaired contraction-stimulated AMPK α 1 activity. This suggests that either AMPK α 1-subunit is dispensable for contraction-stimulated glucose

uptake or the remaining AMPK α 1 activity is sufficient to transduce contraction-stimulated glucose transport. AMPK α 2 appears to be the major isoform recruited for contraction- (Vavvas et al. 1997) or exercise- (Musi et al. 2001) stimulated glucose transport. In contrast, in knock out mice, α 1 but not α 2 mediates contraction-induced glucose uptake (Jorgensen et al. 2004). The identity of the catalytic subunit that specifically participates in contraction-stimulated glucose transport is unclear. The intensity of the contraction protocol may determine AMPK isoform-specific recruitment. Indeed moderate exercise preferentially activates AMPK- α 2 whereas high intensity exercise selectively activates AMPK- α 1 subunit (Fujii et al. 2000, Wojtaszewski et al. 2000). Not surprisingly skeletal muscle glycogen content and fiber type also play a role (Derave et al. 2000). Finally AMPK might not be the sole mediator of contraction-stimulated glucose transport in skeletal muscle (Jorgensen et al. 2004, Mu et al. 2001, Musi et al. 2001).

Table 6. Signaling defects in muscle from animal models of insulin resistance

Insulin signaling defects in PI3K and MAPK cascades account for insulin resistance in animal models of T2DM and obesity. Understanding the metabolic cause of the defects, as well as insulin-independent AMPK and MAPK activation, may prove a resourceful alternative to treat insulin resistance.

(B=basal, I=insulin, P=PMA, C=contraction stimuli; n.d.=not determined. ↑=increased, ↓=decreased, ↔=unchanged compared to insulin-stimulated conditions)

			HIGH FAT	GK	ob/ob	fa/fa
PI 3-K	IR	activ. expr.	↔ ⁽⁸⁾ ↓ ⁽¹⁶⁾ ↔ ⁽⁸⁾	↓ ⁽⁵⁾ ↔ ⁽²¹⁾	↓ ⁽⁷⁾ ↓ ⁽⁷⁾	↓ ⁽¹⁾ ↓ ⁽¹⁾
	IRS-1	activ. ser-P	↓ ⁽¹⁹⁾ ↔ ⁽²³⁾ ↑ ⁽¹⁹⁾	↓ ⁽²¹⁾ ↔ ⁽²⁰⁾	↓ ⁽⁷⁾ ↑ ⁽⁶⁾	↓ ⁽¹⁾ ↑ ⁽⁶⁾
		expr.	↔ ⁽¹⁹⁾	↔ ⁽²¹⁾	↓ ^(7, 18)	↓ ⁽¹⁾
	PI 3-K	activ. expr.	↓ ^(22,24) ↔ ⁽²⁴⁾	↓ ^(12, 21) ↔ ⁽²¹⁾	↓ ^(7,9,22) ↓ ⁽⁷⁾	↓ ⁽²⁾ ↓ ⁽¹⁾
		PKB	activ. expr.	↓ ^(22,23) ↔ ⁽²²⁾	↓ ⁽¹⁵⁾ ↔ ⁽¹²⁾ ↔ ⁽¹⁵⁾	↓ ⁽²²⁾ ↔ ⁽²²⁾
	c,nPKC	activ. expr.	ε, δ, θ ↑ ⁽¹⁹⁾ ↔ ⁽¹⁹⁾	↑ ⁽³⁾ θ ↓ ⁽³⁾ ↔ ⁽³⁾ θ ↓ ⁽³⁾	n.d. n.d.	↑α,ε,θ ⁽³⁾ δ ↓ ⁽³⁾ ↔ ⁽³⁾ δ ↓ ⁽³⁾
aPKCζ		activ. expr.	↓ ^(22,23) ↔ ⁽²²⁾	↔ ⁽³⁾ ↓ ⁽¹³⁾ ↔ ⁽³⁾	↓ ⁽²²⁾ ↔ ⁽²²⁾	↔ ⁽³⁾ ↓ ⁽²²⁾ ↔ ⁽³⁾
MAPK	p38	activ. expr.	n.d. n.d.	n.d. n.d.	↑ ^B ↓ ^{I,P,C} (paperII) ↓ (paperII)	↔ ⁽¹⁰⁾ ↔ ⁽¹⁰⁾
	ERK-1/2	activ. expr.	n.d. n.d.	n.d. n.d.	↔ ^B ↓ ^I ↔ ^{P,C} (paperII) ↔ (paperII)	↔ ⁽¹⁰⁾ ↓ ⁽¹⁷⁾ ↔ ⁽¹¹⁾
		JNK	activ. expr.	n.d. n.d.	n.d. n.d.	↓ ^{I,P} ↔ ^C (paperII) ↔ (paperII)
AMPK	AMPK	activ. expr.	n.d. n.d.	n.d. n.d.	n.d. n.d.	↔ ⁽⁴⁾ ↓α1 ↔α2 ↔ ⁽⁴⁾

¹ Anai M. (1998) *Diabetes* **47**, 13-23 ; ² Anai M. (1999) *Diabetes* **48**, 158-169 ; ³ Avignon A. (1996) *Diabetes* **45**, 1396-1404 ; ⁴ Bergeron R (2001) *Diabetes* **50**, 1076-1082 ; ⁵ Dadke SS. (2000) *Biochem. Biophys. Res. Commun.* **274**, 583-589 ; ⁶ Eckel J. (1985) *Endocrinology* **116**, 1529-1534 ; ⁷ Folli F. (1993) *J. Clin. Invest.* **92**, 1787-1794 ; ⁸ Hansen PA. (1998) *J. Biol. Chem.* **273**, 26157-26163 ; ⁹ Heydrick SJ (1993) *J. Clin. Invest.* **91**, 1358-1366 ; ¹⁰ Ivy J. (2004) *Med. Sci. Sports*, 1207-1211 ; ¹¹ Jiang ZY. (1999) *Diabetes* **48**, 1120-1130 ; ¹² Kanoh Y. (2001) *Endocrinology* **142**, 1595-1605 ; ¹³ Kanoh Y. (2000) *J. Biol. Chem.* **275**, 16690-16696 ; ¹⁴ Kim YB. (2000) *Diabetes* **49**, 847-856 ; ¹⁵ Krook A. (1997) *Diabetes* **46**, 2110-2114 ; ¹⁶ Nagy LJ (1990) *Acta Endocrinol Copenh* **122**:361-368; ¹⁷ Osman AA. (2001) *J. Appl. Physiol.* **90**, 454-460 ; ¹⁸ Saad MJA. (1992) *J. Clin. Invest.* **90**, 1839-1849 ; ¹⁹ Schmitz-Peiffer C. (1997) *Diabetes* **46**, 169-178 ; ²⁰ Schmitz-Peiffer C. (2000) *Cell. Sign.* **12**, 583-594 ; ²¹ Song XM. (1999) *Diabetes* **48**, 1-7; ²² Standaert ML. (2004) *J. Biol. Chem.* **279**, 24929-24934 ; ²³ Tremblay F (2001) *Diabetes* **50**, 1901-1910; ²⁴ Zierath JR. (1997) *Diabetes* **46**, 215-233

Insulin signaling defects in PI3K and MAPK pathways account for skeletal muscle insulin resistance in animal models. This may be due to acute and/or chronic exposure to hyperglycemia, hyperinsulinemia, and/or hyperlipidemia. Defects in AMPKα1 activation do not alter either contraction- or hypoxia-stimulated glucose uptake in

skeletal muscle from Zucker *fa/fa* rat. In addition AMPK α 2 activation is intact in response to hypoxia and contraction in an insulin resistant obese animal model. Thus AMPK activation by insulin-independent pathways appears to bypass impaired insulin signaling to glucose transport in insulin resistant states. Since AMPK γ 3 is expressed specifically in glycolytic skeletal muscle, this isoform may offer a therapeutic opportunity for the treatment of skeletal muscle insulin resistance. The AMPK γ 3-subunit displays a naturally occurring missense mutation replacing arginine residue 225 by glutamine (R225Q) that renders the enzyme constitutively active. Functional analysis, as well as biological validation of the mutation is of crucial importance to ascertain AMPK γ 3 as a putative target for the treatment of skeletal muscle insulin resistance. Therefore transgenic mice specifically overexpressing wild type (Tg-Prkag3^{wt}) or R225Q mutated (Tg-Prkag3^{R225Q}) forms of AMPK γ 3 in white muscle, as well as AMPK γ 3 knock out mice (Prkag3^{-/-}) were generated using the classical targeted mutagenesis technology, and the role of AMPK γ 3 in regulating whole body glucose homeostasis was determined.

The AMPK γ 3-R225Q Mutation Leads to a Constitutively Active and Simultaneous AMP-Insensitive Kinase

AMPK is allosterically activated by AMP and covalently phosphorylated by AMPKK (Hardie et al. 1997). Thus two levels of intervention modulate AMPK activation and this dual regulation renders assessment of AMPK activation *in vitro* challenging. In paper IV, the effect of the R225Q mutation on AMPK activity and phosphorylation by upstream AMPKK was determined in Tg-Prkag3^{wt}, Tg-Prkag3^{R225Q} and Prkag3^{-/-} mice following insulin-independent stimulation. Basal-, AICAR- and contraction-stimulated AMPK phosphorylation was similar between genotypes. However phosphorylation of the AMPK target Acetyl CoA Carboxylase (ACC) was elevated under basal conditions and after AICAR stimulation in Tg-Prkag3^{R225Q} mice. Thus the R225Q mutation appears to induce constitutive activation of AMPK. This contrasts observations in mutated pigs harboring the naturally occurring mutation, whereby AMPK activity in crude muscle membranes was found to be diminished (Milan et al. 2000). Thus the initial report suggested that the R225Q mutation might be a loss of function mutation. However identical mutations in Prkag1 (Hamilton et al. 2001) and Prkag2 (Arad et al. 2002) also result in constitutive activation of AMPK with a concomitant loss of AMP regulation.

The R225Q mutation is a gain of function mutation

Chronic activation of AMPK *in vivo* is correlated with an increase in glycogen content in skeletal muscle (Holmes et al. 1999). A glycogen supercompensation phenotype was observed in mutant pigs (Milan et al. 2000) and confirmed in Tg-Prkag3^{R225Q} mice (paper IV). Thus, the R225Q mutation is not a loss of function mutation. The reduced AMPK activity observed in mutant pigs might be due to inhibitory effects of high glycogen on AMPK activation. AMPK β subunits appear to have a glycogen binding domain and may therefore respond to glycogen feedback mechanisms. Consistent with this is the increased basal phosphorylation on Thr¹⁷² observed in AMPK α 2 dominant negative mice (Mu et al. 2001) that might result from

a negative feedback signal that tries to overcome or compensate for the inhibited AMPK activity.

The R225Q mutation leads to AMP insensitivity

To determine whether the R225Q mutation results in loss of AMP binding, AMPK activation was measured in COS cells expressing heterotrimers containing $\alpha 2$, $\beta 2$ and $\gamma 3$ wild type or R225Q mutated subunit. AMPK activity was increased 2-fold in the absence of AMP and not further increased in the presence of increasing concentrations of AMP. Thus the R225Q mutation in $\gamma 3$ similarly to the R70Q mutation in $\gamma 1$ and the R302Q in $\gamma 2$, leads to AMPK constitutive activation and loss of AMP dependency (Adams et al. 2004). Consistent replacement of an arginine residue by a glutamine in the AMP-binding Cystathionine Beta Synthase-1 (CBS1) domain of AMPK γ -subunits might lead to conformational change and subsequent loss of AMP binding. Whether or not direct binding of AMP molecules is altered in the AMPK γ mutants is unclear (Adams et al. 2004).

AMPK and ACC activation are dissociated

Loss of AMP dependency should translate into loss of AICAR dependency. However, ACC phosphorylation was further increased in Tg-Prkag3^{225Q} mice. This might be an indirect effect of the mutation caused by an altered metabolic state (Rubink et al. 2004). In human muscle prolonged exercise results in marked AMPK phosphorylation that is not sufficient to maintain an elevated ACC phosphorylation (Wojtaszewski et al. 2002) suggesting that AMPK and ACC activation can be dissociated. Alternatively, the AMPK $\gamma 3$ -subunit may not directly mediate ACC phosphorylation, as suggested by unaltered phosphorylation in Prkag3^{-/-} mice and unaltered fatty acid oxidation in Tg-Prkag3^{225Q} and Prkag3^{-/-} mice. To date whether $\gamma 1$ or $\gamma 2$ is necessary to mediate AMPK-induced ACC phosphorylation remains undefined.

AMPK $\gamma 3$ -R225Q subunit replaces endogenous $\gamma 3$

The finding of increased AMPK phosphorylation in COS cells transfected with mutant $\alpha 2\beta 2\gamma 3$ heterotrimer does not translate to the *in vivo* situation. To determine whether there is a dilution effect by endogenous $\gamma 3$ or $\gamma 1$ isoforms, relative mRNA and protein expression was measured in glycolytic and oxidative skeletal muscle tissues of wild type, Tg-Prkag3^{wt}, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice. Endogenous $\gamma 3$ tended to decrease in glycolytic (EDL, gastrocnemius and quadriceps) muscle from either Tg-Prkag3^{wt} or Tg-Prkag3^{225Q} mice, whereas expression in oxidative soleus muscle was low and unchanged. In addition $\gamma 1$ mRNA expression was reduced in glycolytic gastrocnemius and quadriceps of either Tg-Prkag3^{wt} or Tg-Prkag3^{225Q} mice, whereas levels in EDL and soleus remain unaltered. Thus the $\gamma 3$ mutant isoform presumably replaces endogenous $\gamma 3$ in transgenic mice overexpressing wild type and mutant $\gamma 3$ isoform. Protein expression analysis reveals that overexpression of the wild type transgene led to an increase in the amount of $\gamma 3$ protein and a concomitant increase in $\alpha 1$, $\alpha 2$, and $\beta 2$ subunits. Conversely, protein expression of the mutant form is challenging to assess by qualitative Western Blot analysis because endogenous and exogenous mutant forms of $\gamma 3$ differ by a single amino acid substitution. However the

mutation is fully dominant and there is no significant difference in glycogen content between pigs expressing 50% or 100% of the mutant form (Milan et al. 2000). Thus AMPK expression in Tg-Prkag3^{225Q} resembles the expression pattern in wild type mice.

The AMPK γ 3-R225Q Mutation Increases Skeletal Muscle Glycogen Content

To determine whether the AMPK γ 3-R225Q mutation leads to glycogen supercompensation in mouse glycolytic muscle, glycogen content was measured in white gastrocnemius from wild type, Tg-Prkag3^{wt}, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice. Glycogen content was similar in wild type, Tg-Prkag3^{wt} and Prkag3^{-/-} mice, independently of gender. In contrast Tg-Prkag3^{225Q} mice exhibit a 2-fold increase in skeletal muscle glycogen content in both male and female mice (figure 6). This confirms the phenotype observed in pigs (Estrade et al. 1993) and establishes a causal relationship between the AMPK γ 3-R225Q mutation and skeletal muscle glycogen accumulation. Human subjects harboring the AMPK γ 2-R302Q mutation also display increased muscle glycogen storage (Arad et al. 2002) that causes the Wolff-Parkinson-White cardiomyopathy syndrome (Gollob et al. 2001). Thus AMPK γ -subunits play a key role in regulating intramuscular glycogen metabolism. The underlying mechanism is undefined. Current investigations suggest that AMPK might be a GS kinase, thereby modulating glycogen accumulation (Wojtaszewski et al. 2003).

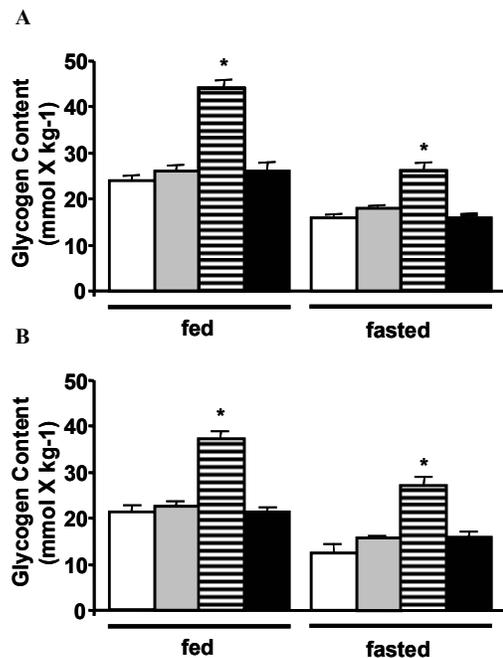


Figure 6. Tg-Prkag3 mice have elevated skeletal muscle glycogen content. Skeletal muscle glycogen content was assessed in fed and fasted male (A) and female (B) mice. Gastrocnemius muscle was excised from wild type (open bar), transgenic wild-type (gray-filled bar), Tg-Prkag3^{225Q} (horizontal lines) and Prkag3^{-/-} (black-filled bar) mice. Glycogen content was assessed fluorometrically. Results are mean \pm SE for 5-30 mice. P<0.01 vs. wild type in the same condition.

Adaptation to chronic exercise is associated with increased glycogen storage (Greiwe et al. 1999). We (paper IV) and others (Andersson 2003) observed that AMPK γ 3 controls the rate of glycogen resynthesis during recovery from exercise. In addition AMPK kinase dead mice have reduced skeletal muscle glycogen content and glycogen resynthesis 3-hr post-exercise (Mu et al. 2003), suggesting that AMPK activation is a determining factor in this process.

Tg-Prkag3^{225Q} and Prkag3^{-/-} Mice Have Normal Growth Rates

Since the AMPK γ 3-R225Q mutation is activating (Andersson 2003), we hypothesized that Tg-Prkag3^{225Q} mice would be protected against diet-induced increase in body weight and adipose tissue accumulation, whereas insulin resistance in the Prkag3^{-/-} mice would be more severe. In paper IV body weight and intraperitoneal adiposity was measured in wild type, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice for 16 weeks.

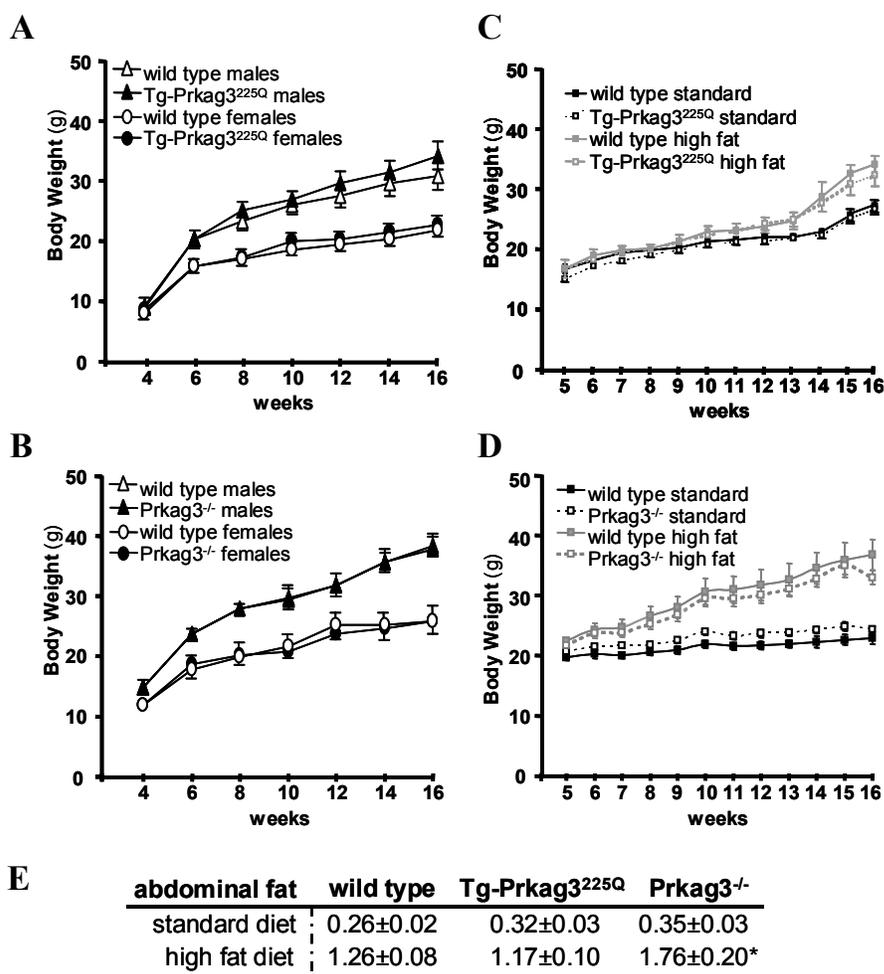


Figure 7. Growth rates are normal in standard and high fat-fed Tg-Prkag3^{225Q} and Prkag3^{-/-} mice. Body weight in male and female Tg-Prkag3^{225Q} (A) and Prkag3^{-/-} mice (B) and standard- (black lines) and high fat- (gray lines) fed Tg-Prkag3^{225Q} (C) and Prkag3^{-/-} mice (D). Results are mean \pm SE for n=8-30 observations. P<0.05 vs. wild type in the same condition.

The R225Q mutation was without effect on body weight and adiposity in female mice, whereas a non significant trend towards increased body weight was observed in male mice (figure 7). Ablation of AMPK γ 3 in Prkag3^{-/-} mice was without effect on growth rates in either gender. Body weight was not measured in Hampshire pigs harboring the R225Q mutation. However increased lean body mass and reduced muscle water content was observed (Milan et al. 2000).

High fat feeding increases body weight and fat accumulation in wild type mice. Body weight is unaltered by either the R225Q mutation or ablation of AMPK γ 3. In contrast intraperitoneal fat accumulation tends to be reduced in Tg-Prkag3^{225Q} mice, whereas Prkag3^{-/-} display a trend for increased intraperitoneal fat mass (figure 7) already under standard diet (non significant). These observations suggest that AMPK γ 3 isoform has a specific role in regulating lipid metabolism, a finding consistent with previously published observations showing that AMPK α 2 knock out mice have increased fat accumulation because of increased TG accumulation in preexisting adipocytes (Villena et al. 2004) despite normal food intake (Viollet et al. 2003).

Glucose-, Insulin- and AICAR-Tolerance are Normal in Tg-Prkag3^{225Q} and Prkag3^{-/-} Mice

The effect of γ 3 ablation and mutant γ 3 overexpression in glycolytic muscle on whole body glucose homeostasis was determined. Tg-Prkag3^{225Q} and Prkag3^{-/-} display normal glucose and insulin tolerance (figure 8A and 8B), consistent with normal glucose tolerance noted in pigs carrying the R225Q mutation (B. Essén-Gustavsson, M. Jensen-Waern, R. Jonasson and L. Andersson, unpublished data). This suggests that the metabolic role of γ 3 is restricted to skeletal muscle, consistent with γ 3 isoform-specific expression in glycolytic muscle (Mahlpuu et al. 2004).

Treatment of diabetic animals with AICAR improves whole body glucose homeostasis (Song et al. 2002) presumably via AMPK activation. We hypothesized that constitutive activation of AMPK in Tg-Prkag3^{225Q} mice leads to enhanced AICAR sensitivity, whereas ablation of γ 3 results in AICAR resistance in skeletal muscle. An AICAR tolerance test was performed in wild type, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice. AICAR tolerance was normal in all mouse models (figure 8C). This finding was unexpected since these animal models display impaired AICAR-stimulated glucose transport (paper IV). The preserved AICAR tolerance might result from AICAR insensitivity in Tg-Prkag3^{225Q} and/or γ 3-independent AICAR effects on fatty acid oxidation. Alternatively, there may be unspecific effects of AICAR on metabolism that override any AMPK-mediated response. The action of AICAR on metabolism is incompletely known and furthermore not restricted to muscle tissue.

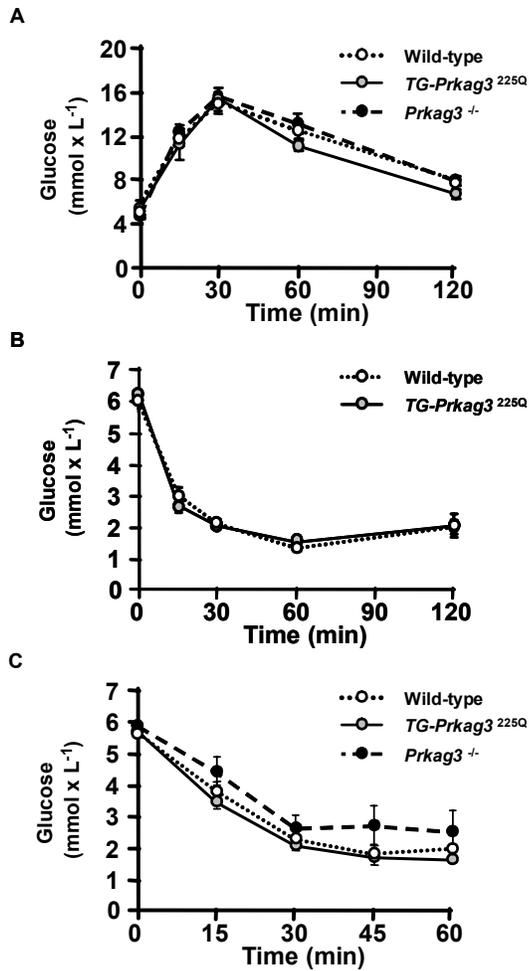


Figure 8. Tg-Prkag3^{225Q} and Prkag3^{-/-} mice have normal glucose, insulin and AICAR tolerance. Glucose (A, 2 g/kg bw), insulin (B, 0.75 mU/kg bw) and AICAR (C, 0.25 g/kg bw) tolerance was assessed in wild type (open circles/dotted line), Tg-Prkag3^{225Q} (gray circles/solid line), and Prkag3^{-/-} (filled circles/dashed line) mice. Glucose tolerance was measured in fasted mice (n=10-15) whereas insulin and AICAR tolerance were measured in fed animals (n=5-8) after an intraperitoneal injection. Thereafter blood glucose was measured at different time points. Insulin tolerance was not assessed in Prkag3^{-/-} mice. Results are mean±SE.

Nutritional Status Controls Insulin Sensitivity in Tg-Prkag3^{225Q} Mice

Although AMPK is not directly regulated by insulin (paper III), it can modulate insulin signaling to glucose transport (Jakobsen et al. 2001). However results showing that AMPK activation leads to increased insulin sensitivity are based on short time (hours or days) activation of the enzyme, whereas the consequence of life long activation, as in genetically engineered mice is unknown. In paper IV, insulin-stimulated glucose transport was determined in mice overexpressing a constitutively active form of AMPK γ 3 in glycolytic skeletal muscle. Tg-Prkag3^{225Q} mice are insulin resistant whereas Prkag3^{-/-} display normal insulin responsiveness (figure 9B). Thus the AMPK γ 3-R225Q mutation can induce skeletal muscle insulin resistance. This might be due to constitutive activation of AMPK on a life-long basis and sustained energy sensing. Consistent with this, insulin resistance was also observed at the level of fatty acid oxidation in Tg-Prkag3^{225Q} mice (figure 10).

Insulin and AMPK have opposing effects on intracellular metabolism in skeletal muscle. Insulin stimulates energy storage, whereas AMPK activation results in increased fuel utilization. Studies aimed to determine the effect of prior insulin or AICAR stimulation on AMPK activation and fuel metabolism reveal prior AMPK activation abolishes insulin's inhibitory effect on fatty acid oxidation (Winder et al. 2000). In addition, contraction markedly blunts insulin-stimulated activation of IRS-1

and PI3K (Goodyear et al. 1995). Thus AMPK activation might lead to insulin resistance. The underlying mechanism might be negative feedback from accumulated intracellular metabolites such as glycogen or lipids. Indeed patients with Mac Ardle's disease (i.e. patients with chronic muscle high glycogen content) exhibit decreased skeletal muscle insulin action (Nielsen et al. 2002). This is consistent with the observation that insulin resistance in Tg-Prkag3^{225Q} mice is lost with fasting (figure 9A) and that the insulin response is unaltered in Prkag3^{-/-} mice. Although the R225Q mutation results in loss of AMP dependency, one can not exclude the possibility that the other intact CBS domains are still AMP sensitive and this may account for a small increase in AMPK activity and subsequent insulin resistance. Thus nutritional status determines insulin resistance in Tg-Prkag3^{225Q} mice and this corresponds to an increased flexibility in signaling that couples metabolic flexibility.

The AMPK γ 3-Subunit is Necessary for AICAR-Induced Glucose Transport

AMPK γ 3-subunit isoform specific involvement in AICAR- and/or contraction-stimulated glucose transport was determined. Specifically, whether the R225Q mutation alters these processes in wild type, Tg-Prkag3^{wt}, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice was addressed.

Independent of nutritional status (i.e. under fasted or fed conditions) AICAR-stimulated glucose transport was significantly reduced in Tg-Prkag3^{225Q} mice, whereas this effect was totally abolished in Prkag3^{-/-} mice (figure 9). This establishes the AMPK γ 3-subunit as a key regulator of AICAR-stimulated glucose transport and confirms that AMPK γ 1- and γ 2-isoforms do not compensate for the loss of γ 3. The observations are consistent with the phenotype observed in AMPK α 2 knock out mice (Jorgensen et al. 2004) and kinase dead form (Mu et al. 2001), since α 2 β 2 γ 3 is the heterotrimer that preferentially associates in Tg-Prkag3^{225Q} mice. Reduced AICAR-stimulated glucose transport in Tg-Prkag3^{225Q} mice might directly be due to increased glycolytic muscle glycogen content (Wojtaszewski et al. 2002). In addition reduced AICAR-stimulated glucose transport in Tg-Prkag3^{225Q} mice is consistent with the loss of AMP sensitivity. AICAR-stimulated glucose transport was not fully abolished in Tg-Prkag3^{225Q} mice compared to Prkag3^{-/-}, thereby suggesting that the mutation might not lead to a total loss of AMP or ATP regulation. This might explain the additional increase in AICAR-induced ACC phosphorylation observed in Tg-Prkag3^{225Q} mice. In contrast to AMPK α 2 knock out mice Tg-Prkag3^{225Q} mice are AICAR tolerant. However the muscle phenotype might be masked by a whole body effect of AICAR on the liver (Bergeron et al. 2001).

Contraction-stimulated glucose transport was similar between all genotypes and this response was preserved in fed and fasted mice. Contraction-stimulated glucose transport was also unaltered in AMPK α 2 knock out mice (Jorgensen et al. 2004) and kinase dead form (Mu et al. 2001), respectively. Thus in our hands changes in skeletal muscle glycogen content do not seem to alter contraction-stimulated glucose transport (Derave et al. 1999, Derave et al., 2000). Altogether these results suggest that an AMPK-independent/contraction-dependent mechanism might also support glucose transport. Intensity and nature of the contraction force generated appears to play a role (Ihlemann et al. 1999, Ihlemann et al. 2000) as well as AMPK α 1-isoform specific involvement in contraction-stimulated glucose transport (Jorgensen et al. 2004).

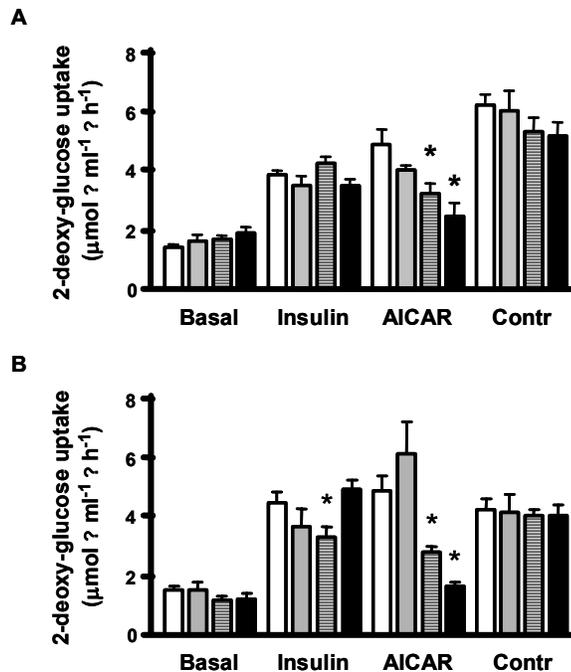


Figure 9. Nutritional status determines insulin- but not AICAR-resistance in Tg-Prkag3^{225Q} mice. Skeletal muscle glucose uptake was assessed in isolated EDL muscle under basal or after stimulation with insulin (12 nM), AICAR (2 mM), or electrically induced contraction (20 Hz for 10 min) in fed (A) or fasted (B) wild type (open bar), Tg-Prkag3^{wt} (gray bar), Tg-Prkag3^{225Q} (horizontal lines), and Prkag3^{-/-} (filled bar) mice. Results are mean±SE for n=4-20 observations. *P<0.05 vs. respective basal.

The AMPK γ 3-Subunit is Dispensable for AICAR-Induced Fatty Acid Oxidation

To test whether AMPK γ 3-isoform is involved in regulating skeletal muscle fatty acid utilization, basal-, insulin- and AICAR-stimulated fatty acid oxidation was determined in wild-type, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice. Fatty acid oxidation under basal conditions was similar between all three genotypes when mice were fed a standard diet. This is consistent with γ 3 playing a major role in glycolytic fibers rather than in oxidative fibers (Mahlpuu et al. 2004).

AICAR relieves insulin inhibition of fatty acid oxidation in skeletal muscle (Kaushik et al. 2001). AICAR-stimulated fatty acid oxidation was similar between genotypes, whereas insulin suppression of fatty acid oxidation was prevented in Tg-Prkag3^{225Q} mice (figure 10). This is consistent with the insulin resistance observed in Tg-Prkag3^{225Q} mice at the level of glucose transport. However results for fatty acid oxidation contrast those for ACC phosphorylation (paper IV) under basal- and AICAR-stimulated conditions, respectively in Tg-Prkag3^{225Q} mice. Recent evidence suggests that concurrent intracellular accumulation of palmitoyl CoA and phosphorylation of ACC by AMPK have stronger effects on ACC inhibition than either alone (Rubink et al. 2004). Similarly, malonyl CoA and phosphorylation of MCD are synergistically regulated (Ruderman et al. 2003). Thus the R225Q mutation might alter intracellular metabolism thereby indirectly controlling fatty acid oxidation. Moreover, dual metabolic and AMPK regulation of ACC and MCD may account for the contrasting

results observed on fatty acid oxidation and ACC phosphorylation. Furthermore there is evidence that AICAR-stimulated ACC phosphorylation and fatty acid oxidation are unrelated. Indeed AICAR-stimulated fat oxidation seems to be dependent on nutritional state, whereas AICAR-induced ACC phosphorylation is unrelated (Kaushik et al. 2001). This suggests that another kinase or phosphatase regulates ACC phosphorylation.

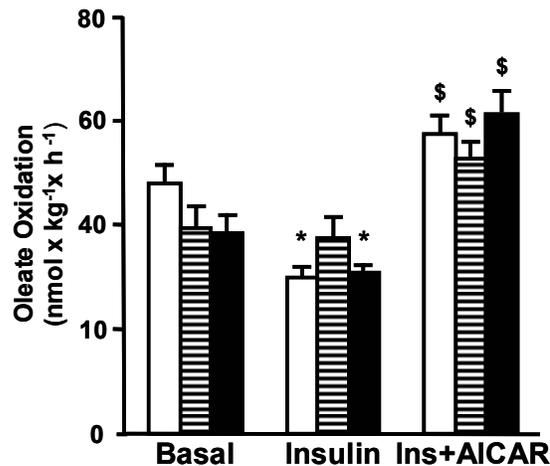


Figure 10. AMPK γ 3 is dispensable for AMPK-stimulated fatty acid oxidation.

Oleate oxidation was assessed in isolated EDL muscle from wild type (open bar), Tg-Prkag3^{225Q} (horizontal lines) and Prkag3^{-/-} (filled bar) mice. Basal oxidation was determined in the presence of 0.3 mM oleate. Insulin (12 nM) was used to suppress oleate oxidation and observe AICAR stimulation. Results are mean \pm SE for n=12-18 observations. *P<0.05 vs. basal; \$P<0.05 vs. insulin.

Fatty acid (FA) oxidation and metabolism are complex processes involving many enzymes. In skeletal muscle lipoprotein Lipase (LPL1) and CD36 allow FA release from circulating TG and FA entry into the myocyte, respectively. Once inside the cell, FA are esterified into FA-Coenzyme A (FA CoA) and either stored back into TG or taken up by the mitochondria via Carnitine Palmitoyl Transferase (CPT1) for oxidation. Once in the mitochondria, FA-CoA can either be exported back to the cytosol via Uncoupling Protein (UCP3) or enter the tricarboxylic acid cycle following stepwise action of Hydroxy-Acetyl CoA Dehydrogenase (HAD) and citrate synthase (CS) to generate acetyl CoA and citrate, respectively. Thus multiple levels of regulation are to be considered. AMPK has been postulated to regulate gene expression and mitochondrial biogenesis (Zong et al. 2002). Thus mitochondrial function and associated lipid metabolism were determined in wild type, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice by investigating relative mRNA expression of LPL1, CD36, CPT1, UCP3, HAD and CS. In Tg-Prkag3^{225Q} mice skeletal muscle CD36, UCP3 and CS were increased, whereas LPL1, CPT1 and HAD were unchanged. These observations suggest that the R225Q mutation alters lipid metabolism. Increased CS gene expression might explain the increased ACC phosphorylation noted in Tg-Prkag3^{225Q} mice (Vavvas et al. 1997). Indeed increased FA oxidation is associated with increased ACC phosphorylation and subsequent ACC inactivation. In contrast, mitochondrial gene expression in Prkag3^{-/-} mice appears to be normal (figure 14). Thus the combined effect of the R225Q

mutation and subsequent altered metabolism might indirectly affect muscle mitochondrial biogenesis.

Thus the heterotrimeric complex formed by α 2-, β 2- and γ 3-AMPK isoforms is dispensable for skeletal muscle fatty acid oxidation. However the R225Q mutation in combination with lipid oversupply appears to significantly alter mitochondrial function but this does not translate to altered fatty acid oxidation when mice are standard-fed. Challenging the mice with high fat diet might reveal such a phenotype.

The AMPK γ 3-R225Q Mutation Protects Against Diet-Induced Skeletal Muscle Insulin Resistance

To test whether Tg-Prkag3^{225Q} mice are protected against diet-induced skeletal muscle insulin resistance, wild-type, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice were challenged with a 55% fat-containing diet for 12 weeks and metabolic consequences were assessed (paper IV). High fat feeding does not alter the glycogen phenotype conferred by the mutation (figure 11). However TG was increased in skeletal muscle from high fat-fed wild-type and Prkag3^{-/-} mice, thereby providing a mechanism for the concomitant insulin resistance developed in these models. Fatty acid oxidation is reduced in wild-type but not in Prkag3^{-/-} mice, consistent with the indirect role that the γ 3-subunit might play in this process.

On the other hand high fat feeding did not alter the glycogen phenotype conferred by the mutation. However, intramuscular TG content is not increased in Tg-Prkag3^{225Q} mice when fed a high fat diet. Accumulation of TG on the high fat diet is prevented by the increase in fatty acid oxidation in Tg-Prkag3^{225Q} mice, suggesting that these mice oxidize more lipids. This is consistent with the phenotype observed in mutant Hampshire pigs, whereby oxidative capacity is increased (Estrade et al. 1994, Lebret, 1999 #237, Milan, 2000 #185). Indeed, AMPK activation mediates the lipid lowering effect of Metformin in skeletal muscle and liver (Zang et al. 2004) and activation of AMPK enhances sensitivity of muscle glucose transport to insulin (Fisher et al. 2002).

High fat feeding leads to a surprising reduction in CPT-1, HAD, CS and UCP3 in Tg-Prkag3^{225Q} mice compared to standard-fed mice (figure 14). Whether this translates functionally at the level of changes in protein expression is currently unknown. Thus, under conditions where the lipid supply is increased, the R225Q mutation downregulates mitochondrial biogenesis. Nevertheless, reduced gene expression is a marker for later reduction in expression of functional proteins. Conceivably, the 12 weeks period of high fat feeding is the point at which the mutant mice are unable to compensate at the mitochondrial level. One interesting observation is that LPL1 and CD36 were also reduced, which suggests that the skeletal muscle might be in an overloaded energetic state that results in selective fatty acid directing towards the adipose tissue. However, abdominal fat accumulation as measured by fat mass in Tg-Prkag3^{225Q} mice was unchanged compared to wild-type mice. Nevertheless, the R225Q mutation might confer increased skeletal muscle metabolic flexibility that allows intracellular fuel redirection towards increased utilization. This is particularly evident when mice are fed a high fat diet and of great interest since lipid oversupply precipitates the appearance of insulin resistance and T2DM.

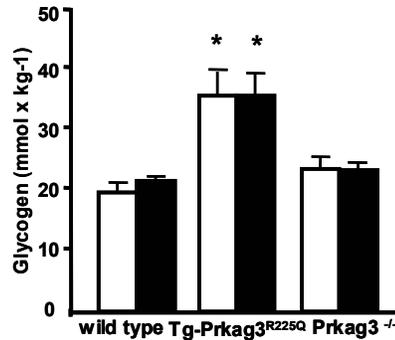


Figure 11. High fat feeding does not alter muscle glycogen content in Tg-Prkag3^{R225Q} and Prkag3^{-/-} mice. Muscle glycogen content was measured in fed female mice. Gastrocnemius muscle was excised from standard (open bar) or high fat (closed bar) –fed wild type, Tg-Prkag3^{R225Q} and Prkag3^{-/-} mice. Results are mean±SE for 8-10 observations. P<0.01 vs. wild type in the same condition.

The AMPK γ 3-R225Q Mutation Does Not Protect Against Diet-Induced Whole Body Insulin Resistance

The effect of the R225Q mutation on whole body glucose homeostasis was determined by a glucose tolerance test. Tg-Prkag3^{R225Q} mice are not protected against diet induced glucose intolerance. Indeed high fat-fed Tg-Prkag3^{R225Q} mice are glucose intolerant and this might be due to increased hepatic TG content (figures 12 and 13). In addition, the AMPK γ 3-subunit does not appear to modulate hepatic energetic status since Prkag3^{-/-} mice have normal liver TG. Thus AMPK γ 3-subunit specifically regulates energy status in glycolytic skeletal muscle, whereby it prevents lipid-induced insulin resistance. AMPK has been suggested to play a central role in regulating energy homeostasis. AMPK α 2^{-/-} mice display whole body insulin resistance that results from increased sympathetic tone, rather than impaired skeletal muscle insulin sensitivity (Violet et al. 2003). The current understanding is that central regulation of AMPK opposes peripheral insulin action (Andersson et al. 2004). In other words, AMPK activation in the hypothalamus results in hyperphagia and insulin resistance in rats (Namkoong et al. 2005), whereas AMPK activation prevents diet-induced muscle insulin resistance in transgenic mice. Thus the role of tissue specific isoforms becomes of paramount importance and caution must be made when modulating AMPK activity at the whole body level.

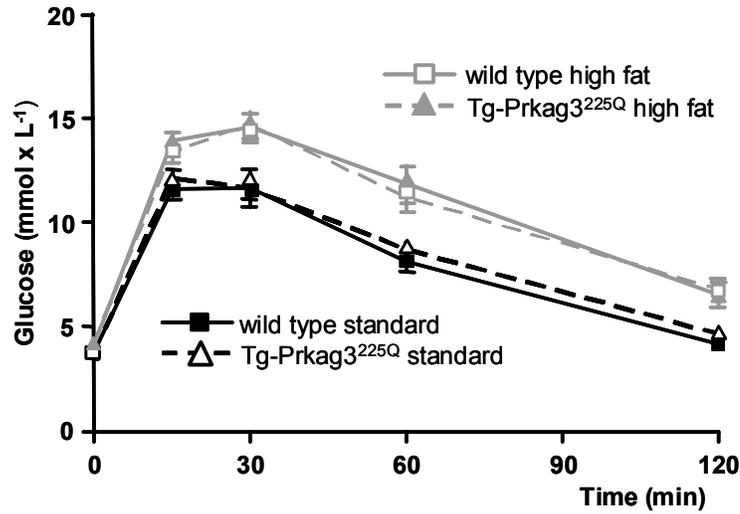


Figure 12. High fat fed Tg-Prkag3^{R225Q} mice are glucose intolerant. Glucose (2 g/kg bw) tolerance was assessed in wild type (square/solid line) and Tg-Prkag3^{R225Q} (triangle/dashed line) fed a standard (black lines) or high fat (gray lines) diet for 12 weeks. Thereafter blood glucose was measured at 15, 30, 60 and 120 min. Results are mean±SE for n=15-20 mice.

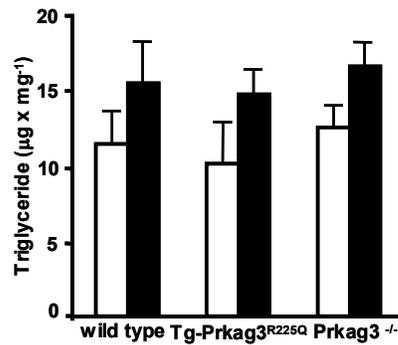


Figure 13. High fat feeding does not alter liver triglyceride content in Tg-Prkag3^{R225Q} and Prkag3^{-/-} mice. Liver triglyceride content was measured in fed mice. Gastrocnemius muscle was excised from standard- (open bar) or high fat- (closed bar) fed wild type, Tg-Prkag3^{R225Q} and Prkag3^{-/-} mice. Results are mean±SE for 4-6 observations.

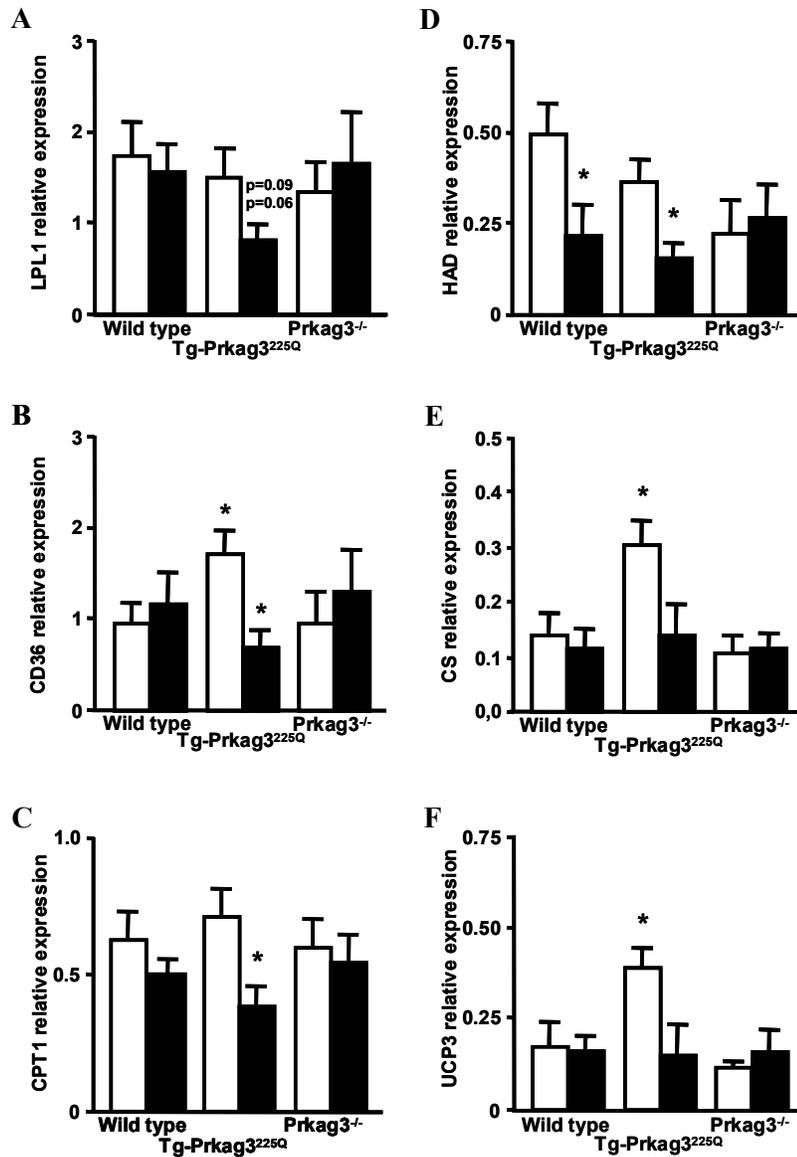


Figure 14. Lipid gene expression is upregulated in standard and downregulated in skeletal muscle from high fat fed Tg-Prkag3^{225Q} mice.

Relative mRNA expression of LPL1 (A), CD36 (B), CPT-1 (C), HAD (D), CS (E) and UCP-3 (F). Gastrocnemius muscle was excised for RNA extraction and purification. Quantification of mRNA was performed using real-time PCR with the ABI PRISM 7700 Sequence Detector System. Data is expressed relative to endogenous 36B4 gene. Results are mean±SE for n=6-10 observations. For B, C and D: P<0.05 vs. standard on same genetic background. For E and F: P<0.05 vs. wild type on same diet. For A: P=0.09 vs. wild type on the same diet and P=0.06 vs. standard on same genetic background.

Strategies to Prevent Skeletal Muscle Insulin Resistance

Skeletal muscle insulin resistance is an important pathophysiological feature of T2DM and therefore a major site of action for therapeutic strategies. Directly modulating, or bypassing defective insulin signaling may provide a mechanism to increase GLUT4 translocation to the plasma membrane and subsequent glucose transport in skeletal muscle, with the ultimate goal of restoring glucose homeostasis. Glucose transport and gene regulatory responses to GLUT4 translation are activated following insulin-dependent and -independent stimuli. In diabetic GK rat insulin-dependent PI3K signaling is defective whereas ERK1/2 response is intact. In contrast obese Zucker *fa/fa* and *ob/ob* rodents exhibit insulin resistance in PI3K and MAPK signaling, respectively. Thus dyslipidemia leads to more profound defects on insulin intracellular signaling compared to hyperglycemia. Indeed glucose may contribute to impair insulin-stimulated PI3K signaling via direct modulation of PDK-1 and PKC isoforms whereas ERK1/2 is not regulated by glucose. In addition defects in IR number and activation in morbidly obese but not hyperglycemic states, might explain defective PI3K and MAPK signaling in obese animal models. Strategies aimed to improve defective insulin signaling may prove useful for the treatment of insulin resistance in T2DM, but may be more challenging to treat insulin resistance in morbid obesity. Conversely, intact insulin-independent activation of MAPK and AMPK signaling in skeletal muscle from insulin resistant severely obese Zucker *fa/fa* rats suggests that MAPK and AMPK offer potential sites of pharmacological intervention for the regulation of glucose homeostasis. Functional analysis of AMPK γ 3-specific subunit shows that AMPK activation prevents diet-induced skeletal muscle insulin resistance and provides biological validation for AMPK as a potential therapeutic target for the treatment of insulin resistance.

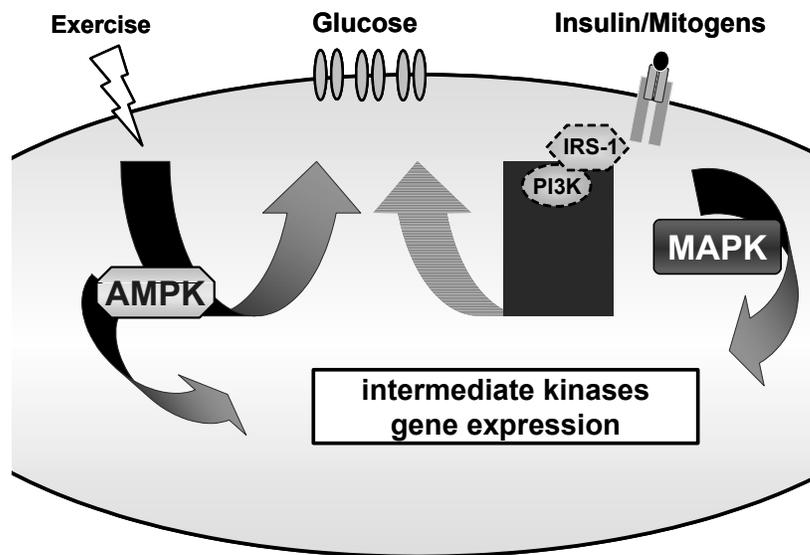


Figure 15. AMPK and MAPK: potential therapeutic targets

SUMMARY

- Insulin-stimulated defects in PI3K and PKB are not reversed by acute euglycemia and may account for skeletal muscle insulin resistance in non-obese diabetic GK rats.
- In skeletal muscle, glucose directly activates PDK-1 and downstream PKC isoforms (α/β , δ and ζ) phosphorylation through a mechanism that is independent of changes in PI3K, PKB and ERK1/2 activation.
- Insulin induces a robust increase in ERK1/2, p38-MAPK and JNK phosphorylation in a similar time- and dose-dependent manner.
- Insulin-stimulated p38-MAPK and JNK phosphorylation occur in a glycolytic skeletal muscle fiber-type-specific manner, whereas insulin-stimulated ERK1/2 phosphorylation is indistinguishable between oxidative and glycolytic fibers.
- PMA and contraction significantly increase phosphorylation of all three MAPK modules. The combined effect of insulin and contraction on p38-MAPK is reduced, whereas no additivity is observed for JNK and ERK1/2 phosphorylation.
- Insulin and PMA elicit additive effects on JNK and ERK1 phosphorylation, whereas ERK2 and p38-MAPK are phosphorylated by a kinase presumably activated by insulin and PMA signaling pathways.
- Defects in MAPK signaling account for skeletal muscle insulin resistance in *ob/ob* mice, whereas contraction- and PMA-stimulated ERK1/2 and JNK phosphorylation are unaffected by obesity driven insulin resistance.
- Reduced p38-MAPK expression may account for skeletal muscle insulin resistance in *ob/ob* mice since functional defects are observed in response to insulin-dependent and insulin-independent stimuli.
- In Zucker *fa/fa* rat hypoxia- and contraction-stimulated glucose transport and AMPK α 2 activation is preserved in skeletal muscle despite severe insulin resistance.
- Contraction-stimulated AMPK α 1 isoform specific defect in skeletal muscle from Zucker *fa/fa* rats is inconsequential for glucose transport activity.
- The predominant heterotrimeric AMPK complex accounting for activity contains AMPK α 2 β 2 γ 3 subunits.

- The AMPK γ 3 R225Q missense mutation is an activating mutation that results in increased glycolytic muscle glycogen content.
- The AMPK γ 3 isoform is required for AICAR-stimulated glucose transport but is dispensable for AICAR-stimulated fatty acid oxidation.
- The AMPK γ 3 R225Q mutation protects against dietary-induced skeletal muscle insulin resistance via a mechanism that prevents intramuscular triglyceride accumulation and subsequent insulin resistance, via enhanced fatty acid oxidation.

CONCLUSIONS and FUTURE PERSPECTIVES

This thesis was directed towards identifying signaling defects in PI3K and MAPK pathways that underlie skeletal muscle insulin resistance in diabetic GK rats and *ob/ob* mice. In addition insulin-independent activation of MAPK and AMPK pathways were also investigated in order to determine whether exercise-, stress- and PMA-mediated signaling cascades to glucose transport and mitogenic responses could potentially bypass defective insulin signaling in insulin resistant *ob/ob* and Zucker *fa/fa* rodents. Finally AMPK was validated as a potential target for pharmacological intervention to treat skeletal muscle insulin resistance associated with T2DM and obesity.

The mechanisms underlying glucose-induced insulin resistance is complex and appears to depend upon time and concentration factors. Mild chronic hyperglycemia, as in diabetic GK rats, impairs insulin signaling at the level of PI3K and PKB, whereas acute high glucose exposure directly modulates PDK-1 and PKC. In addition, acute euglycemia in rats chronically exposed to mild or elevated plasma glucose concentrations normalizes PKB and PKC ζ , but not PI3K activation. Thus glucose effects on PKC occur within hours and are reversible, whereas PKB defects require longer exposure to mild or elevated glucose concentrations and normalization occurs within days. Finally the regulation of PI3K is independent of glycemia. To date, PKC isoforms are the only established players in hyperglycemia-induced insulin resistance. A clearer picture of isoform specific PKC dysregulation following hyperglycemia is emerging.

Glucose-induced PDK-1 activation is a key finding of this thesis. Exposure of skeletal muscle to elevated glucose concentration rapidly results in a shift in glucose metabolism towards increased storage and reduced utilization. This is very interesting in light of the glucose effects on PKB and glycogen metabolism. PDK-1 may regulate glycogen metabolism independently of PKB via GSK3 under acute hyperglycemic conditions. A better understanding of PDK-1 regulation *in vivo* is needed. To date PDK-1 defects in insulin resistant states have not been identified, however, this thesis implicated PDK-1 as a glucose-regulated target.

MAPK modules are multiproteic complex whose organization allow for transduction and/or amplification of highly specialized signals. Distinguishing the activation of distinct MAPK following extracellular stimuli is challenging. The activating mechanisms upstream of MEKK are largely undefined. Specificity in signaling might come from the distinct receptors recruited. Receptors for insulin-independent stimuli including exercise and stress are undescribed, which makes it challenging to delineate the molecular mechanisms upstream of MEKK activation. The combined effect of insulin and contraction does not elicit additive effects on JNK and ERK1/2 phosphorylation. Similarly no additivity was observed for insulin- and PMA-stimulated ERK2 and p38-MAPK phosphorylation. Thus PMA- and contraction-stimuli may share common signaling cascades with insulin to activate some but not all MAPK. Finally identification of fast twitch fiber-specific insulin-stimulated activation of p38-MAPK and JNK signaling raises the possibility of a fiber-type specific activation of MAPK on insulin sensitivity.

Contraction-stimulated ERK1/2, JNK and AMPK activation in morbidly obese insulin resistant *ob/ob* and Zucker *fa/fa* rodents is intact. Thus the signaling pathway

activated by contraction is preserved in severely insulin resistant states. Understanding the underlying mechanisms becomes of paramount importance to identify potential sites of pharmacological intervention. Differences in isoform-specific AMPK catalytic subunit activation following distinct *in vitro* contraction and *in vivo* exercise protocols may reveal selectivity in the AMPK signaling pathway. In addition understanding changes in intracellular energy status following exercise/contraction may prove informative.

Isoform-specific multimeric composition of signal transducers, as well as subsequent intracellular specialized function, is key information to specific and better drug targeting. AMPK- $\alpha 2\beta 2\gamma 3$ is the predominant heterotrimer active in glycolytic muscle *in vivo*. Functional analysis of the R225Q mutation in the AMPK $\gamma 3$ -isoform reveals modification of AMPK to a constitutively active kinase. The R225Q mutation in the AMPK $\gamma 3$ isoform alters skeletal muscle glycogen content, thereby suggesting a key role of this subunit in glucose intracellular metabolism. Understanding the underlying mechanism for AMPK-induced glycogen accumulation is essential to understand the effect of the mutation. One hint is the possibility that AMPK directly binds to glycogen via a glycogen-binding domain on its β regulatory subunit.

Finally AMPK $\gamma 3$ -R225Q mutation prevents skeletal muscle, but not whole body diet-induced insulin resistance. The R225Q mutation increases lipid oxidation in the presence of lipid oversupply, which attenuates the expected accumulation of intramuscular TG content. However hepatic TG accumulation was similar between wild type, Tg-Prkag3^{225Q} and Prkag3^{-/-} mice, thereby providing a mechanism for impaired glucose tolerance in Tg-Prkag3^{225Q} mice. Central and peripheral AMPK regulations oppose themselves. This, along with tissue-specific AMPK heterotrimeric composition, is key information to prevent concurrent increased peripheral tissue fuel utilization and food intake. Especially since increased food intake together with a sedentary life style contribute to the development of T2DM.

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